

	M	K	L	Q	C	V	S	L	W	9
GAATTCCGACAAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC	ATG	AAG	TTA	CAG	TGT	GTT	TCC	CTT	TGG	69
L	L	G	T	I	L	I	L	C	S	29
CTC	CTG	GGT	ACA	ATA	CTG	ATA	TTG	TGC	TCA	129
	GTA	GAC	AAC	CAC	GGT	CTC	AGG	AGA	TGT	
I	S	T	D	M	H	H	I	E	E	49
ATT	TCC	ACA	GAC	ATG	CAC	CAT	ATA	GAA	GAG	189
	AGT	TTC	CAA	GAA	ATC	AAA	AGA	GCC	ATC	
A	K	D	T	F	P	N	V	T	I	69
GCT	AAG	GAC	ACC	TTC	CCA	AAT	GTC	ACT	ATC	249
	CTG	TCC	ACA	TTG	GAG	ACT	CTG	CAG	ATC	
K	P	L	D	V	C	C	V	T	K	89
AAG	CCC	TTA	GAT	GTG	TGC	TGC	GTG	ACC	AAG	309
	AAC	CTC	CTG	GCG	TTC	TAC	GTG	GAC	AGG	
F	K	D	H	Q	E	P	N	P	K	109
TTC	AAG	GAT	CAT	CAG	GAG	CCA	AAC	CCC	AAA	369
	ATC	TTG	AGA	AAA	ATC	AGC	AGC	ATT	GCC	
S	F	L	Y	M	Q	K	T	L	R	129
TCT	TTC	CTC	TAC	ATG	CAG	AAA	ACT	CTG	CGG	429
	CAA	TGT	CAG	GAA	CAG	AGG	CAG	TGT	CAC	
R	Q	E	A	T	N	A	T	R	V	149
AGG	CAG	GAA	GCC	ACC	AAT	GCC	ACC	AGA	GTC	489
	ATC	CAT	GAC	AAC	TAT	GAT	CAG	CTG	GAG	
H	A	A	A	I	K	S	L	G	E	169
CAC	GCT	GCT	GCC	ATT	AAA	TCC	CTG	GGA	GAG	549
	CTC	GAC	GTC	TTT	CTA	GCC	TGG	ATT	AAT	
N	H	E	V	M	S	S	A	*		178
AAT	CAT	GAA	GTA	ATG	TCC	TCA	GCT	TGA		576
TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACTGTGGGAGACAGCCCACCTTGAAGGG										655
GAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCCCACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGC										734
CAAAAAGTCTACTGTGGTATTTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGC										813
CTTCCCATCTAATTTATTGTGAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCTGTAGTACACATTGT										892
ACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGAAAAAAAAAAAAAAAAAAAAACCAGCTGAGCGCCGG										971
TCGCTACCAAAGCCGAATTC										991

Fig. 1

	1					50
il10-human	~MHSSALLCC	LVLLTGVRAS	PGQGTQSENS	CTHFPGNLPN	MLRDLRDAFS	
il10-mouse	~MPGSALLCC	LLLLTGMRIS	RGQYSREDNN	CTHFPVGQSH	MLLELRDAFS	
il10-viral	~MFRASLLCC	LVLLAGVWAD	NKYDSESGDD	CPTLPTSLPH	MLHELRAAFS	
mda7-mouse	MSWGLQILPC	LSLILLWNQ	VPGLEGQEFR	FGSCQV.TGV	VLPELWEAFW	
mda7-human	~~MQMVVLPC	LGFTLLWSQ	VSGAQGQEFH	FGPCQV.KGV	VPQKLWEAFW	
italy	~~~~MKLQC	VSLWLL.GT	ILILCSVDNH	GLRRCL.IST	DMHHIEESFQ	
Consensus	-M-GSALLCC	L-LLL--WA-	VG-LSG-ENH	C-H-PV-L--	MLHELREAFS	
	51					100
il10-human	RVKTFFQMKD	QLDN..LLLK	ESLLEDFKGY	LGCQALSEMI	QFYLEEVMPO	
il10-mouse	QVKTFQTKD	QLDN..ILLT	DSLMDQDFKGY	LGCQALSEMI	QFYLVEMPO	
il10-viral	RVKTFFQMKD	QLDN..MLLD	GSLLEDFKGY	LGCQALSEMI	QFYLEEVMPO	
mda7-mouse	TVKNTVQTQD	DITSIRLLKP	.QVLRNVSGA	ESCYLAHSL	KFYLNVTVFN	
mda7-human	AVKDTMQAQD	NITSARLLQQ	.EVLQNVSDA	ESCYLVHTLL	EFYLVTVFN	
italy	EIKRAIQAKD	TFPNVTILST	LETQIIKPL	DVCCVTKNLL	AFYVDRVFKD	
Consensus	RVKTFFQ-KD	QLDN-RLLLT	-SLQDFKGY	LGCQALSE--	QFYLEEV--Q	
	101					150
il10-human	AENQDPD..I	KAHVNSLGEN	LKTLRLRLRR	CHRFLPCENK	SKAVEQ...V	
il10-mouse	AEKHGPE..I	KEHLNSLGEK	LKTLRMRLRR	CHRFLKCENK	SKAVEQ...V	
il10-viral	AENHSTD.QE	KDKVNSLGEK	LKTLRVRLRR	CHRFLPCENK	SKAVEQ...V	
mda7-mouse	YHSKIAKFKV	LRSFSTLANN	FIVIMSQLOP	SKDNSMLPIS	ESAHQRFLLF	
mda7-human	YHNRTVEVRT	LKSFSTLANN	FVLIVSQLOP	SQENEMFSIR	DSAHRRFLLF	
italy	HQE..PNPKI	LRKISSIANS	FLYMOKTLRQ	CQEQRQCHCR	QEATNATRVI	
Consensus	AENH-P--KI	-R---SL--N	-KTLRSRLRR	CHRFL-CENK	SKAVEQFLLV	
	151					187
il10-human	KNAFNKLQ.E	KGIYKAMSEF	DIFINYIEAY	MTMKIRN		
il10-mouse	KSDFNKLQ.D	QGVYKAMNEF	DIFINCIEAY	MMIKMKS		
il10-viral	KSAFSKLQ.E	KGVYKAMSEF	DIFINYIEAY	MTTKMKN		
mda7-mouse	RRTFKQLDTE	VALVKAFGEV	DILLTWMQKF	YHL~~~~		
mda7-human	RRAFKQLDVE	AALTKALGEV	DILLTWMQKF	YKL~~~~		
italy	HDNYDQLEVH	AAAIKSLGEL	DVFLAWINKN	HEVMSSA		
Consensus	K-AF--L-VE	---YKAMGEF	DIF-NWIE-Y	MTLKMKN		

Fig. 2

cgtccgccac gcgtccggac tagttetaga tcgcgagcgg ccgccctttt tttttttttt 60  
ttggaagtcc taggactgat ctccaggacc agcactcttc tcccagccct tagggctctg 120  
ctcggccaag gccttccttg cc atg cga cct gtc agt gtc tgg cag tgg agc 172  
ccc tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct 220  
ccg tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt 268  
cgg ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg 316  
gag ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc 364  
acg ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag 412  
gcc aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc 460  
atc tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act 508  
gaa tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag 556  
gat gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac 604  
tcc aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga 652  
att cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag 700  
ggg ctg gtg gaa gtc agg ctt cct gac ggc tgg tcg caa gtg tgc gac 748  
aaa ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc 796  
ttc ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc 844  
caa cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc 892  
acg gag gcc cac ctc tcc ctc tgt tcc ctg gag ttc tat cgt gcc aat 940  
gac acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg 988  
cca ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag 1036  
tcg aag cct cag ggg gag gcc cgt gtc cgt cta aag ggc ggc gcc cac 1084  
cct gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca 1132  
gtc tgt gac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg 1180  
gag ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg 1228  
ggg cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga 1276

Fig. 3A

cag gag ctc tcc ctc tgg aag tgc ccc cac aag aac atc aca gct gag	1324
gat tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac	1372
act ggg gca gag acc agg atc cga ctc agt ggg ggc cgc agc caa cat	1420
gag ggg cga gtc gag gtg caa ata ggg gga cct ggg ccc ctt cgc tgg	1468
ggc ctc atc tgt ggg gat gac tgg ggg acc ctg gag gcc atg gtg gcc	1516
tgt agg caa ctg ggt ctg ggc tac gcc aac cac ggc ctg cag gag acc	1564
tgg tac tgg gac tct ggg aat ata aca gag gtg gtg atg agt gga gtg	1612
cgc tgc aca ggg act gag ctg tcc ctg gat cag tgt gcc cat cat ggc	1660
acc cac atc acc tgc aag agg aca ggg acc cgc ttc act gct gga gtc	1708
atc tgt tct gag act gca tca gat ctg ttg ctg cac tca gca ctg gtg	1756
cag gag acc gcc tac atc gaa gac cgg ccc ctg cat atg ttg tac tgt	1804
gct gcg gaa gag aac tgc ctg gcc agc tca gcc cgc tca gcc aac tgg	1852
ccc tat ggt cac cgg cgt ctg ctc cga ttc tcc tcc cag atc cac aac	1900
ctg gga cga gct gac ttc agg ccc aag gct ggg cgc cac tcc tgg gtg	1948
tgg cac gag tgc cat ggg cat tac cac agc atg gac atc ttc act cac	1996
tat gat atc ctc acc cca aat ggc acc aag gtg gct gag ggc cac aaa	2044
gct agt ttc tgt ctc gaa gac act gag tgt cag gag gat gtc tcc aag	2092
cgg tat gag tgt gcc aac ttt gga gag caa ggc atc act gtg ggt tgc	2140
tgg gat ctc tac cgg cat gac att gac tgt cag tgg att gac atc acg	2188
gat gtg aag cca gga aac tac att ctc cag gtt gtc atc aac cca aac	2236
ttt gaa gta gca gag agt gac ttt acc aac aat gca atg aaa tgt aac	2284
tgc aaa tat gat gga cat aga atc tgg gtg cac aac tgc cac att ggt	2332
gat gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc	2380
cag acc agc aac cag att atc taagtgccac tgccctctgc aaaccaccac	2431
tggccctctaa tggcaggggt ctgaggctgc cattacctca ggagcttacc aagaaacca	2491
tgtcagcaac cgcactcatc agaccatgca ctatggatgt ggaactgtca agcagaagtt	2551

Fig. 3B

ttcaccctcc ttcagaggcc agctgtcagt atctgtagcc aagcatggga atctttgctc 2611  
ccaggcccag caccgagcag aacagaccag agcccaccac accacaaaga gcagcacctg 2671  
actaactgcc cacaaaagat ggcagcagct cattttcttt aataggaggt caggatgggtc 2731  
agctccagta tctcccctaa gtttaggggg atacagcttt acctctagcc ttttggtggg 2791  
ggaaaagatc cagccctccc acctcatttt ttactataat atgttgctag gtataatttt 2851  
attttatata aaaagtgttt ctgtgattct tcagaaaaaa aaaaaaaaaa aaaaaaaaaa 2911  
aaaaaaaaa 2920

Fig. 3C

6/68

Met	Arg	Pro	Val	Ser	Val	Trp	Gln	Trp	Ser	Pro	Trp	Gly	Leu	Leu	Leu			
1				5					10					15				
Cys	Leu	Leu	Cys	Ser	Ser	Cys	Leu	Gly	Ser	Pro	Ser	Pro	Ser	Thr	Gly			
			20					25					30					
Pro	Glu	Lys	Lys	Ala	Gly	Ser	Gln	Gly	Leu	Arg	Phe	Arg	Leu	Ala	Gly			
		35					40					45						
Phe	Pro	Arg	Lys	Pro	Tyr	Glu	Gly	Arg	Val	Glu	Ile	Gln	Arg	Ala	Gly			
	50					55					60							
Glu	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Asp	Phe	Thr	Leu	Gln	Ala	Ala	His			
65				70						75					80			
Ile	Leu	Cys	Arg	Glu	Leu	Gly	Phe	Thr	Glu	Ala	Thr	Gly	Trp	Thr	His			
				85					90					95				
Ser	Ala	Lys	Tyr	Gly	Pro	Gly	Thr	Gly	Arg	Ile	Trp	Leu	Asp	Asn	Leu			
		100						105					110					
Ser	Cys	Ser	Gly	Thr	Glu	Gln	Ser	Val	Thr	Glu	Cys	Ala	Ser	Arg	Gly			
		115					120					125						
Trp	Gly	Asn	Ser	Asp	Cys	Thr	His	Asp	Glu	Asp	Ala	Gly	Val	Ile	Cys			
	130					135					140							
Lys	Asp	Gln	Arg	Leu	Pro	Gly	Phe	Ser	Asp	Ser	Asn	Val	Ile	Glu	Val			
145					150					155				160				
Glu	His	His	Leu	Gln	Val	Glu	Glu	Val	Arg	Ile	Arg	Pro	Ala	Val	Gly			
				165					170					175				
Trp	Gly	Arg	Arg	Pro	Leu	Pro	Val	Thr	Glu	Gly	Leu	Val	Glu	Val	Arg			
			180					185					190					
Leu	Pro	Asp	Gly	Trp	Ser	Gln	Val	Cys	Asp	Lys	Gly	Trp	Ser	Ala	His			
		195					200					205						
Asn	Ser	His	Val	Val	Cys	Gly	Met	Leu	Gly	Phe	Pro	Ser	Glu	Lys	Arg			
	210					215					220							
Val	Asn	Ala	Ala	Phe	Tyr	Arg	Leu	Leu	Ala	Gln	Arg	Gln	Gln	His	Ser			
225					230					235					240			
Phe	Gly	Leu	His	Gly	Val	Ala	Cys	Val	Gly	Thr	Glu	Ala	His	Leu	Ser			
				245					250					255				
Leu	Cys	Ser	Leu	Glu	Phe	Tyr	Arg	Ala	Asn	Asp	Thr	Ala	Arg	Cys	Pro			
			260					265					270					

Fig. 4A

Gly	Gly	Gly	Pro	Ala	Val	Val	Ser	Cys	Val	Pro	Gly	Pro	Val	Tyr	Ala	
		275					280					285				
Ala	Ser	Ser	Gly	Gln	Lys	Lys	Gln	Gln	Gln	Ser	Lys	Pro	Gln	Gly	Glu	
	290					295					300					
Ala	Arg	Val	Arg	Leu	Lys	Gly	Gly	Ala	His	Pro	Gly	Glu	Gly	Arg	Val	
305					310					315					320	
Glu	Val	Leu	Lys	Ala	Ser	Thr	Trp	Gly	Thr	Val	Cys	Asp	Arg	Lys	Trp	
				325					330					335		
Asp	Leu	His	Ala	Ala	Ser	Val	Val	Cys	Arg	Glu	Leu	Gly	Phe	Gly	Ser	
			340					345					350			
Ala	Arg	Glu	Ala	Leu	Ser	Gly	Ala	Arg	Met	Gly	Gln	Gly	Met	Gly	Ala	
		355					360					365				
Ile	His	Leu	Ser	Glu	Val	Arg	Cys	Ser	Gly	Gln	Glu	Leu	Ser	Leu	Trp	
	370					375					380					
Lys	Cys	Pro	His	Lys	Asn	Ile	Thr	Ala	Glu	Asp	Cys	Ser	His	Ser	Gln	
385					390					395					400	
Asp	Ala	Gly	Val	Arg	Cys	Asn	Leu	Pro	Tyr	Thr	Gly	Ala	Glu	Thr	Arg	
				405					410					415		
Ile	Arg	Leu	Ser	Gly	Gly	Arg	Ser	Gln	His	Glu	Gly	Arg	Val	Glu	Val	
			420					425					430			
Gln	Ile	Gly	Gly	Pro	Gly	Pro	Leu	Arg	Trp	Gly	Leu	Ile	Cys	Gly	Asp	
		435					440					445				
Asp	Trp	Gly	Thr	Leu	Glu	Ala	Met	Val	Ala	Cys	Arg	Gln	Leu	Gly	Leu	
	450					455					460					
Gly	Tyr	Ala	Asn	His	Gly	Leu	Gln	Glu	Thr	Trp	Tyr	Trp	Asp	Ser	Gly	
465					470					475					480	
Asn	Ile	Thr	Glu	Val	Val	Met	Ser	Gly	Val	Arg	Cys	Thr	Gly	Thr	Glu	
				485					490					495		
Leu	Ser	Leu	Asp	Gln	Cys	Ala	His	His	Gly	Thr	His	Ile	Thr	Cys	Lys	
			500					505					510			
Arg	Thr	Gly	Thr	Arg	Phe	Thr	Ala	Gly	Val	Ile	Cys	Ser	Glu	Thr	Ala	
		515					520					525				
Ser	Asp	Leu	Leu	Leu	His	Ser	Ala	Leu	Val	Gln	Glu	Thr	Ala	Tyr	Ile	
	530					535					540					

Fig. 4B

Glu	Asp	Arg	Pro	Leu	His	Met	Leu	Tyr	Cys	Ala	Ala	Glu	Glu	Asn	Cys	
545					550					555					560	
Leu	Ala	Ser	Ser	Ala	Arg	Ser	Ala	Asn	Trp	Pro	Tyr	Gly	His	Arg	Arg	
				565					570					575		
Leu	Leu	Arg	Phe	Ser	Ser	Gln	Ile	His	Asn	Leu	Gly	Arg	Ala	Asp	Phe	
			580					585					590			
Arg	Pro	Lys	Ala	Gly	Arg	His	Ser	Trp	Val	Trp	His	Glu	Cys	His	Gly	
		595					600					605				
His	Tyr	His	Ser	Met	Asp	Ile	Phe	Thr	His	Tyr	Asp	Ile	Leu	Thr	Pro	
	610					615					620					
Asn	Gly	Thr	Lys	Val	Ala	Glu	Gly	His	Lys	Ala	Ser	Phe	Cys	Leu	Glu	
625					630					635					640	
Asp	Thr	Glu	Cys	Gln	Glu	Asp	Val	Ser	Lys	Arg	Tyr	Glu	Cys	Ala	Asn	
				645					650					655		
Phe	Gly	Glu	Gln	Gly	Ile	Thr	Val	Gly	Cys	Trp	Asp	Leu	Tyr	Arg	His	
			660					665					670			
Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	Ile	Thr	Asp	Val	Lys	Pro	Gly	Asn	
		675					680					685				
Tyr	Ile	Leu	Gln	Val	Val	Ile	Asn	Pro	Asn	Phe	Glu	Val	Ala	Glu	Ser	
	690					695					700					
Asp	Phe	Thr	Asn	Asn	Ala	Met	Lys	Cys	Asn	Cys	Lys	Tyr	Asp	Gly	His	
705					710					715					720	
Arg	Ile	Trp	Val	His	Asn	Cys	His	Ile	Gly	Asp	Ala	Phe	Ser	Glu	Glu	
				725					730					735		
Ala	Asn	Arg	Arg	Phe	Glu	Arg	Tyr	Pro	Gly	Gln	Thr	Ser	Asn	Gln	Ile	
			740					745					750			
Ile																
753																

Fig. 4C



atgcgacctg tcagtgtctg gcagtggagc ccctgggggc tgctgctgtg cctgctgtgc 60  
agttcgtgct tgggggtctcc gtccccttcc acggggccctg agaagaaggc cgggagccag 120  
gggcttcggt tccggctggc tggcttcccc aggaagccct acgagggccg cgtggagata 180  
cagcgagctg gtgaatgggg caccatctgc gatgatgact tcacgctgca ggctgcccac 240  
atcctctgcc gggagctggg cttcacagag gccacaggct ggacccacag tgccaaatat 300  
ggccctggaa caggccgcat ctggctggac aacttgagct gcagtgggac cgagcagagt 360  
gtgactgaat gtgcctcccg gggctggggg aacagtgact gtacgcacga tgaggatgct 420  
ggggctcatct gcaaagacca gcgcctccct ggcttctcgg actccaatgt cattgaggta 480  
gagcatcacc tgcaagtgga ggaggtgca attcgaccgc ccgttgggtg gggcagacga 540  
cccctgcccg tgacggaggg gctgggtgga gtcaggcttc ctgacggctg gtcgcaagtg 600  
tgcgacaaag gctggagcgc ccacaacagc cacgtggtct gcgggatgct gggcttcccc 660  
agcgaaaaga ggggtcaacgc ggccttctac aggctgctag cccaacggca gcaacactcc 720  
tttggctctgc atgggggtggc gtgcgtgggc acggaggccc acctctccct ctgttccctg 780  
gagttctatc gtgccaatga caccgccagg tgccctgggg ggggccctgc agtgggtgagc 840  
tgtgtgccag gccctgtcta cgcggcatcc agtggccaga agaagcaaca acagtccaag 900  
cctcaggggg agggccgtgt ccgtctaaag ggcggcgccc accctggaga gggccgggta 960  
gaagtccctga agggccagcac atggggcaca gtctgtgacc gcaagtggga cctgcatgca 1020  
gccagcgtgg tgtgtcggga gctgggcttc gggagtgtc gagaaactct gaggggcgct 1080  
cgcatggggc agggcatggg tgctatccac ctgagtgaag ttcgctgtc tggacaggag 1140  
ctctccctct ggaagtgcc ccacaagaac atcacagctg aggattgttc acatagccag 1200  
gatgccgggg tccgggtgcaa cctaccttac actggggcag agaccaggat ccgactcagt 1260  
ggggggccgca gccaacatga ggggcgagtc gaggtgcaaa tagggggacc tgggcccctt 1320  
cgctggggcc tcactctgtg ggatgactgg gggaccctgg aggccatggt ggcctgtagg 1380  
caactgggtc tgggctacgc caaccacggc ctgcaggaga cctggtactg ggactctggg 1440  
aatataacag aggtggtgat gagtggagtg cgctgcacag ggactgagct gtccctggat 1500

Fig. 5A

cagtgtgccc atcatggcac ccacatcacc tgcaagagga cagggacccg cttcactgct 1560  
ggagtcatct gttctgagac tgcatacagat ctgttgctgc actcagcact ggtgcaggag 1620  
accgcctaca tcgaagaccg gcccttgc atgttgtact gtgctgcgga agagaactgc 1680  
ctggccagct cagcccgtc agccaactgg ccctatggtc accggcgtct gctccgattc 1740  
tcctcccaga tccacaacct gggacgagct gacttcaggc ccaaggctgg gcgccactcc 1800  
tggggtgtggc acgagtgcc tgggcattac cacagcatgg acatcttcac tcactatgat 1860  
atcctcacc ccaatggcac caaggtggct gagggccaca aagctagttt ctgtctcgaa 1920  
gacactgagt gtcaggagga tgtctccaag cggtatgagt gtgccaaactt tggagagcaa 1980  
ggcatcactg tgggttgctg ggatctctac cgcatgaca ttgactgtca gtggattgac 2040  
atcacggatg tgaagccagg aaactacatt ctccaggttg tcatcaacct aaactttgaa 2100  
gtagcagaga gtgactttac caacaatgca atgaaatgta actgcaaata tgatggacat 2160  
agaatctggg tgcacaactg ccacattggt gatgccttca gtgaagaggc caacaggagg 2220  
tttgaacgct accctggcca gaccagcaac cagattatc 2259

Fig. 5B

11/68

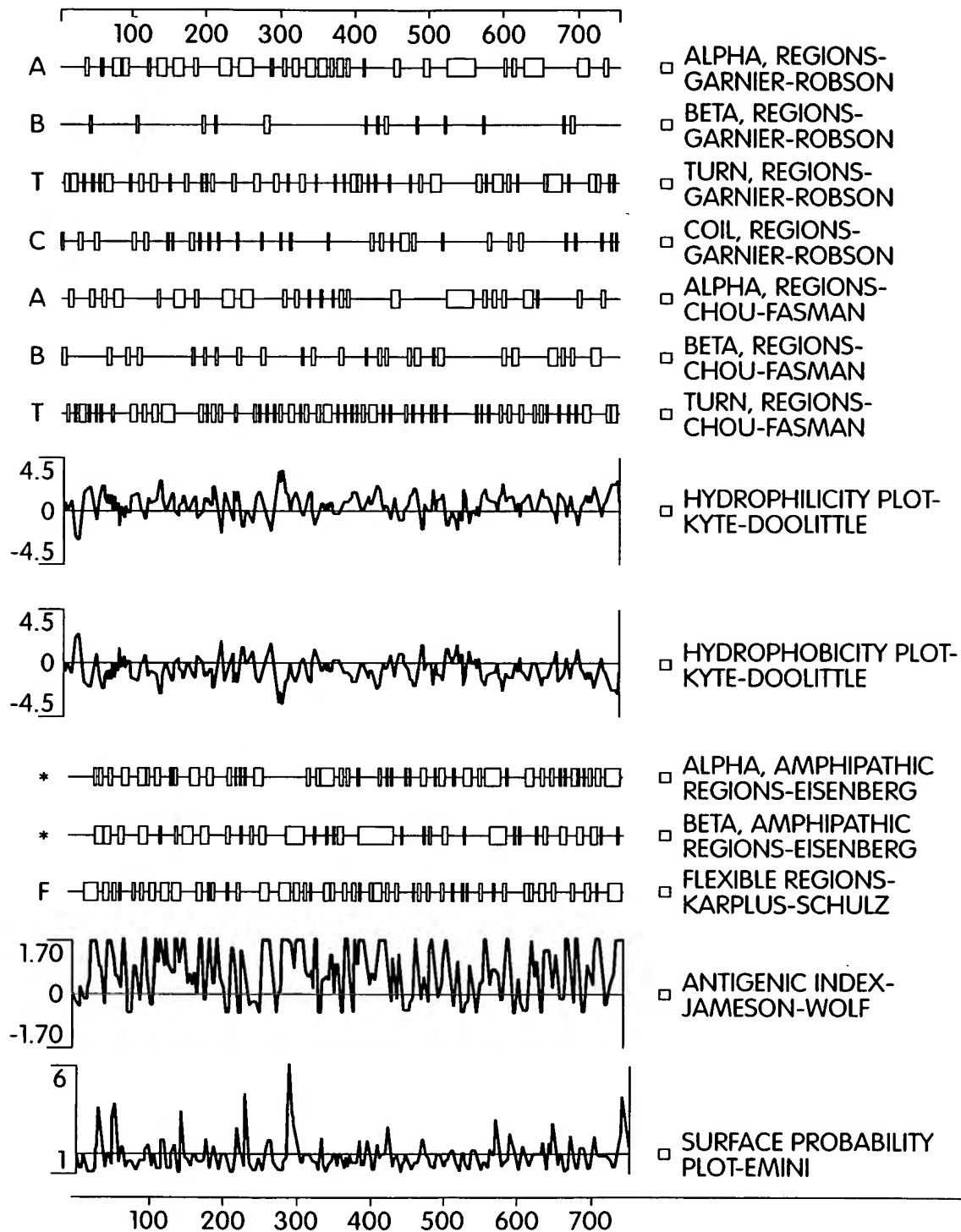


Fig. 6

12/68

	1	60
LOX	MRFA-----WTVLLLGPLQ-----LCALVHCAPPAAGQQQP-----	
huLOL	MALA-----RGSRLGALV-----WGACLCVHVH-----GQQAQ-----	
huLor	MERPLCSHLCSCLAAMLALLSPLSLAQYDSWPHYPEYFQQPAPEYHQPAQANVAKIQLRL	
muLor-2	M-RAVSVMWYCCPWGLLLHCL-C-----SFSVGSPPSPS-ISPEKKVGSQGLRFRL	
huLor-2	M-RPVSVWQWSPWGLLL--CLLC-----SSCLGSPSPS-TGPEKKAGSQGLRFRL	
	61	120
LOX	---PREPPAAPGAWRQQIQWENN-GQVFSL-----LSLGSQY-----	
huLOL	---P-GQGSDDPARWRQLIQWENN-GQVYSL-----LNSGSEYVPA-----GPQRSESSSR	
huLor	AGQKRKHSEGRVEVYYDGWGTVCDDDFSIIHAAHVVCRELGYVEAKSWTASSSYGKGEGP	
muLor-2	AGFPRKPYEGRVEIQRAGEWGTICDDDFTLQAAHVLCRELGFTEATGWTHSAKYGPGTGR	
huLor-2	AGFPRKPYEGRVEIQRAGEWGTICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGR	
	121	180
LOX	-----QPQRRRDPGAA-----VPG---AANASAOQPRTP	
huLOL	VLLA-----GAPQAQQRSHGSPRRRQAPSLP-----LPG-RVGSDTVRGQARHP	
huLor	IWLNLHCTGNEATLAACTSNGWGVTDCKHTEDVGVVCSDKRIPGFKFDNSLINQIENLN	
muLor-2	IWLNLSCRGTEGTSVTECASRGWGNSDCTHDEDAQVICKDQRLPGF--SDSNVIEVEH-Q	
huLor-2	IWLNLSCSGTEQSVTECASRGWGNSDCTHDEDAQVICKDQRLPGF--SDSNVIEVEH-H	
	181	240
LOX	ILL--IRD---N-----RTAAG-----RTRTAGSSGVTAG-----	
huLOL	FGFGQVPD---NWREVAVGDSTGMALARTSVS-----QQRHGGSSASSVSAS-AFAST-	
huLor	IQVEDIRIRAILSTYRKRTPVMEGYVEVKEGKTWKQICDKHWTAKNSRVVCGMFGFPGER	
muLor-2	LQVEEVRLRPAVEWGRRPLPVTEGLVEVRLPEGWSQVCDKGWSAHNSHVVCMLGFPGEK	
huLor-2	LQVEEVRLRPAVGWGRRPLPVTEGLVEVRLPDGWSQVCDKGWSAHNSHVVCMLGFPSEK	
	241	300
LOX	-----RP-RPTARHWF-----QAGY-----STSR	
huLOL	-----YRQ-QPSYPQQFPY-----PQAPF---VSQYENYDPASRT	
huLor	TYNTKVYKNFASRRKQRYWPFMSDCTGTEAHISSCKLGPQVSLDPMKNVTCENGLPAVVS	
muLor-2	RVNMAFYRMLAQKKQHSFGLHSVACVGTEAHLSLCSLE---FYRANDTTRCSGGNPAVVS	
huLor-2	RVNAAFYRLLAQRRQHSFGLHGVACVGTEAHLSLCSLE---FYRANDTARCPGGGPVAVVS	
	301	360
LOX	-----REAGPSR---AENQTAPGEVPAL-----SNLRP	
huLOL	YDQGFVY-----YRPAGGGV---GAGAAAVASAGVI-----YPYQP	
huLor	CVPGQVFSPDGPSRFRKAYKPE-QPLVRLRGGAYIGEGRVEVLKNGEWGTVCDKDWDLVS	
muLor-2	CVLGPLYATFTGQKKQQHSPQGEARVRLKGGAHQGEGRVEVLKAGTWGTVCDRKWDLQA	
huLor-2	CVPGPVYAASSGQKKQQQSKPQGEARVRLKGGAHQGEGRVEVLKASTWGTVCDRKWDLHA	
	361	420
LOX	PS-----RVDGMVGDD-----PYNP-----	
huLOL	RA-----RYEEYGGGEELPEYPPQG---FYAPAPERPYVPPPPPPPD	
huLor	ASVVCRELGFGSAKEAVTGSRLGQIGIPIHLNEIQCTGNEKSIIDCKFNA-ESQGCNHEE	
muLor-2	ASVVCPDELGFGTAREALSGARMGQMGAIHLSEVRCSGQEPSLWRCPSKNI TAEDCSHSQ	
huLor-2	ASVVCRELGFGSAREALSGARMGQMGAIHLSEVRCSGQELSLWKCPHKNI TAEDCSHSQ	

Fig. 7A

	421	480
LOX	-----YK---YSDDNPPYNYDYTYERPRPG-----GRYRP-----GYGTG	
huLOL	<u>GLDRRYSHSLYSEGTPGFE--QAYDPDPGEAAQAHGGDPRLGWYPPYANP--PPEAYGPP</u>	
huLor	<u>DAGVRCNTP-AMGLQKKLRLNGGRNPYEGRVEVLVERNGLVWGMVCGQNWGIVEAMVVC</u>	
muLor-2	<u>DAGVRCNLP-YTGIVETKIRLSGGRSRYEGRVEVQIGIPGHLRWGLICGDDWGTLEAMVAC</u>	
huLor-2	<u>DAGVRCNLP-YTGAETRIRLSGGRSQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVAC</u>	
	481	540
LOX	-----Y-----FQ-----Y	
huLOL	<u>RALEPPY-----LPVRSSDTPPPGGE-----RNGAQQGRLSVGSVY</u>	
huLor	<u>RQLGLGFASNAFQETWYWHGDVNSNKVVMMSGVKCSGTLSLAHCRHDGEDVACPQGGVQY</u>	
muLor-2	<u>RQLGLGYANHGLQETWYWDG-NVTEVVMGVRCTGSELSLNQCAHHSSHITCKKTGTRF</u>	
huLor-2	<u>RQLGLGYANHGLQETWYWDG-NITEVVMGVRCTGTLSLDQCAHHGTHITCKRTGTRF</u>	
	541	600
LOX	-----GLPDLVADPYYIQASTYVQKMSMYNLRCAAEEENCLASTAYRADVRDYDHRVL	
huLOL	<u>RPNQN-GRGLPDLVPDPNYVQASTYVQRAHLYSLRCAAEEKCLASTAYAPEATDYDVRVL</u>	
huLor	<u>GAGVACSETAPDLVLNAEMVQQTYYLEDPRMFMLQCAMEENCLSASAAQTD-PTTGYYRL</u>	
muLor-2	<u>TAGVICSETASDLLLHLSALVQETAYIEDRPLHMLYCAAEEENCLASSARSAN-WPYGHRRL</u>	
huLor-2	<u>TAGVICSETASDLLLHLSALVQETAYIEDRPLHMLYCAAEEENCLASSARSAN-WPYGHRRL</u>	
	601	660
LOX	<u>LRFPQRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQORRAEGHKAS</u>	
huLOL	<u>LRFPQRVKNQGTADFLPNRPRHTWEWHSCHQHYHSMDEFSHYDLLDAATGKKVAEGHKAS</u>	
huLor	<u>LRFSSQIHNNQSDFRPKNGRHAWIWHDCRHRYHSMFVTHYDLLNLN-GTKVAEGHKAS</u>	
muLor-2	<u>LRFSSQIHNLGRADFRPKAGRHSWWHECHGHYHSMDFTHYDILTPN-GTKVAEGHKAS</u>	
huLor-2	<u>LRFSSQIHNLGRADFRPKAGRHSWWHECHGHYHSMDFTHYDILTPN-GTKVAEGHKAS</u>	
	661	720
LOX	<u>FCLEDTSCDYGYHRRFACTAHT-QGLSPGCYDTYGADIDCQWIDITDVKPGNYILKVSVN</u>	
huLOL	<u>FCLEDSTCDFGNLKRYACTSHT-QGLSPGCYDTYNADIDCQWIDITDVQPGNYILKVHVN</u>	
huLor	<u>FCLEDTECEGDIQKNYECANFGDQGITMGCWDMYRHDIDCQWVIDITDVPPGDYLFQVVIN</u>	
muLor-2	<u>FCLEDTECQEDVSKRYECANFGEOGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVIN</u>	
huLor-2	<u>FCLEDTECQEDVSKRYECANFGEOGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVIN</u>	
	721	779
LOX	<u>PSYLVPESDYTNNVVRCDIRYTGHAYASGCTI-----SPY</u>	
huLOL	<u>PKYIVLESDFTNVVRNCNIHYTGRYVSATNCKI-----VQS</u>	
huLor	<u>PNFEVAESDYSNNIMKCRSRYDGHRIWMYNCHIGGSFSEETEKKFEHFSGLLNNQLSPQ</u>	
muLor-2	<u>PNFEVAESDFTNNAMKCCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQIV--</u>	
huLor-2	<u>PNFEVAESDFTNNAMKCCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQII--</u>	

Fig. 7B

14/68

RADIATION HYBRIDS STATS, P = 0.0001

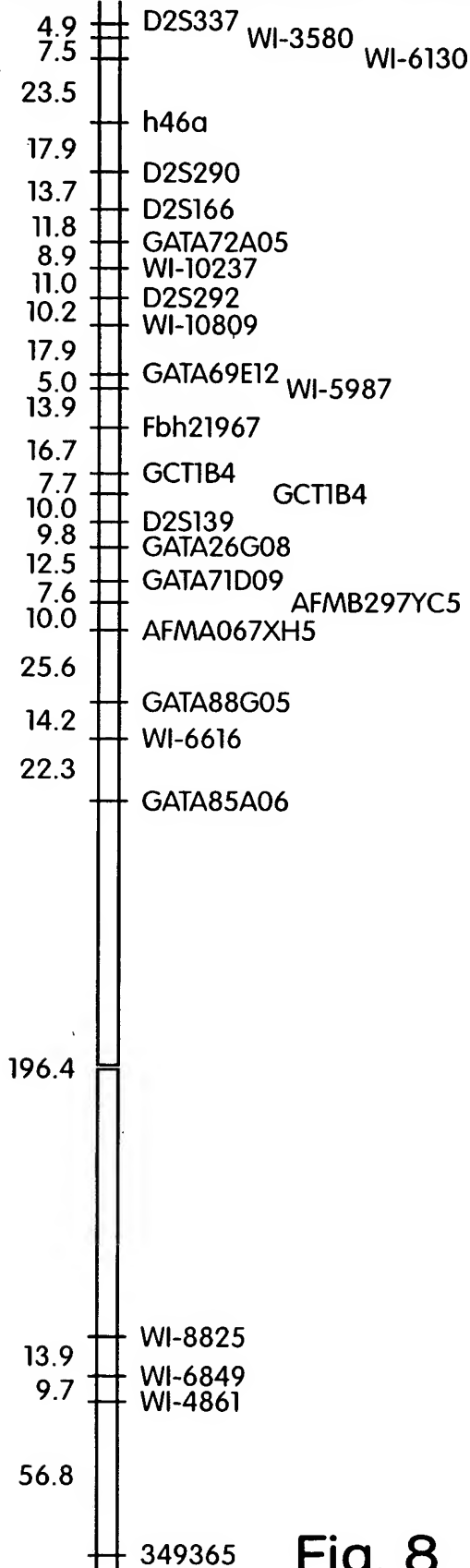


Fig. 8

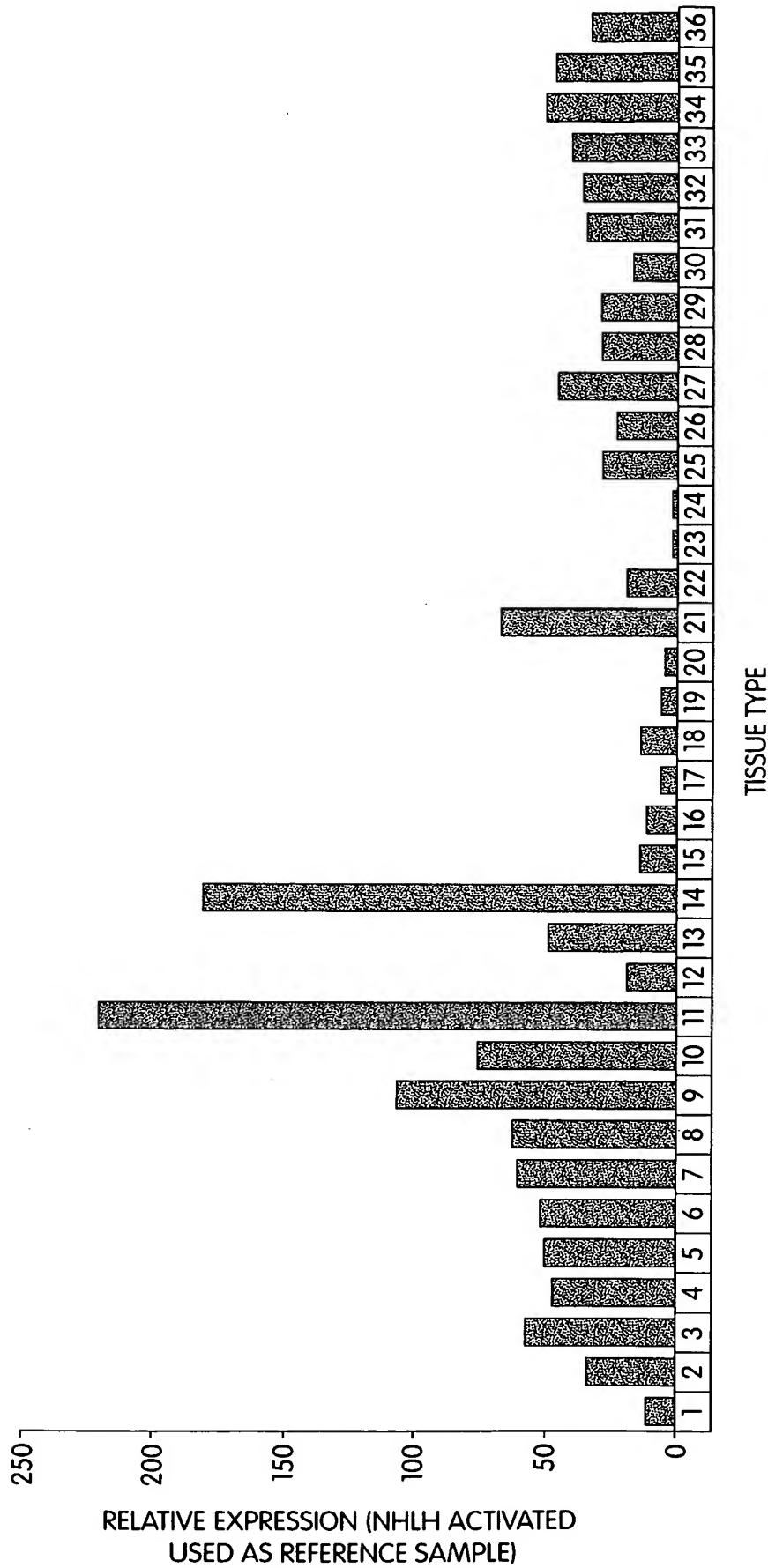


Fig. 9

16/68

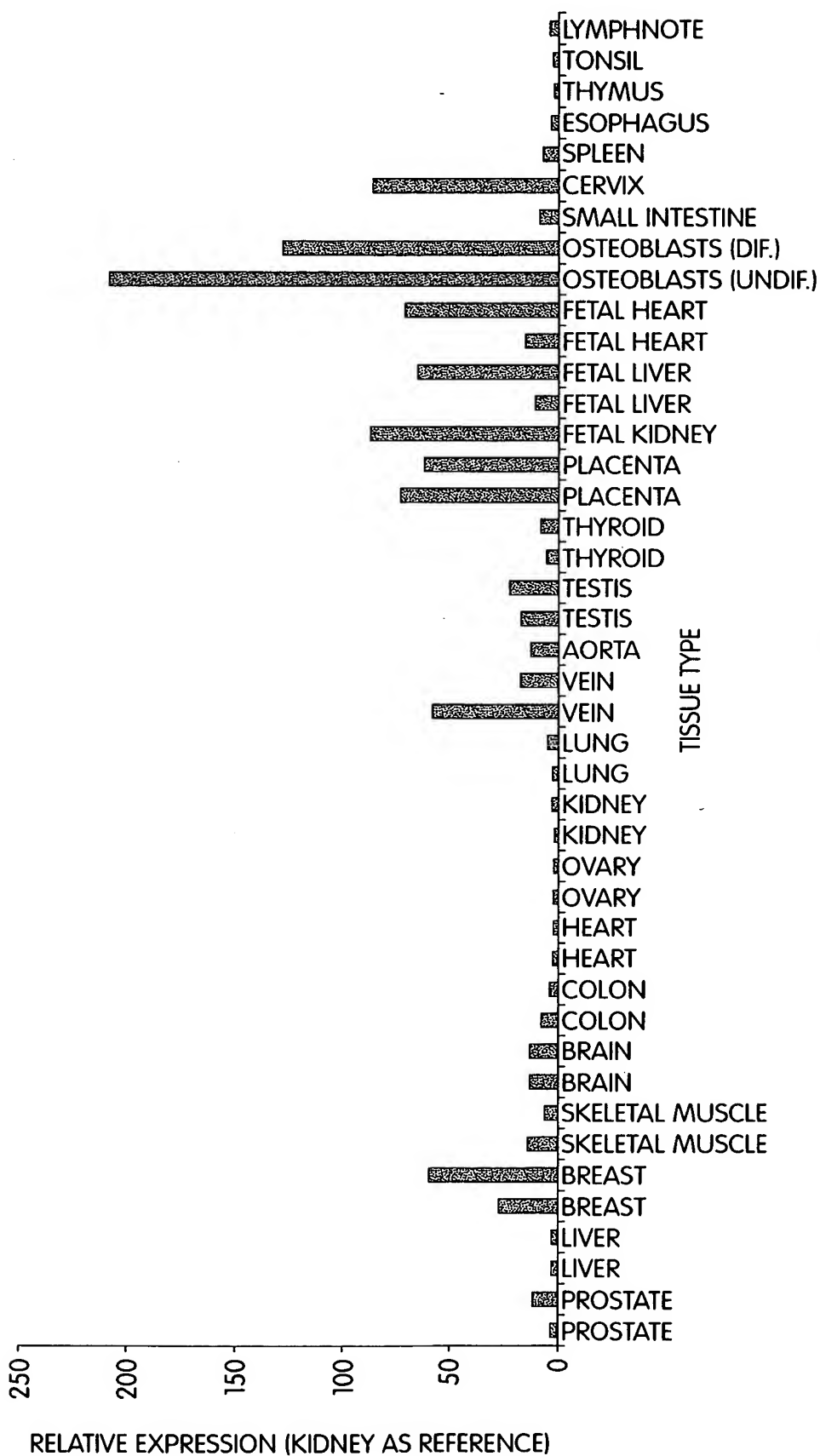


Fig. 10





Fig. 11

GAATTTCGGCACGAGGGCCGGCACCCCCGCGCCACCCAGCCTCAAACCTGCAGTCCGGCGCCGCGGGGCAGGACAAGGGG 79

M A L K V L P L H R T V L 13  
AAGGAATAAACACGTTTGGTGAGAGCC ATG GCA CTC AAG GTC CTA CCT CTA CAC AGG ACG GTG CTC 145

F A A I L F L L H L A C K V S C E T G D 33  
TTC GCT GCC AIT CTC TTC CTA CTC CAC CTG GCA TGT AAA GTG AGT TGC GAA ACC GGA GAT 205

C R Q Q E F K D R S G N C V L C K Q C G 53  
TGC AGG CAG CAG GAA TTC AAG GAT CGA TCT GGA AAC TGT GTC CTC TGC AAA CAG TGC GGA 265

P G M E L S K E C G F G Y G E D A Q C V 73  
CCT GGC ATG GAG TTG TCC AAG GAA TGT GGC TTC GGC TAT GGG GAG GAT GCA CAG TGT GTG 325

P C R P H R F K E D W G F Q K C K P C A 93  
CCC TGC AGG CCG CAC CGG TTC AAG GAA GAC TGG GGT TTC CAG AAG TGT AAG CCA TGT GCG 385

D C A L V N R F Q R A N C S H T S D A V 113  
GAC TGT GCG CTG GTG AAC CGC TTT CAG AGG GCC AAC TGC TCA CAC ACC AGT GAT GCT GTC 445

C G D C L P G F Y R K T K L V G F Q D M 133  
TGC GGG GAC TGC CTG CCA GGA TTT TAC CGG AAG ACC AAA CTG GTT GGT TTT CAA GAC ATG 505

Fig. 12A

E	C	V	P	C	G	D	P	P	P	P	Y	E	P	H	C	T	S	K	V	153
GAG	TGT	GTG	CCC	TGC	GGA	GAC	CCA	CCT	CCT	CCC	TAC	GAA	CCA	CAC	TGT	ACC	AGC	AAG	GTG	565
N	L	V	K	I	S	S	T	V	S	S	P	R	D	T	A	L	A	A	V	173
AAC	CTT	GTG	AAG	ATC	TCC	TCC	ACC	GTC	TCC	AGC	CCT	CGG	GAC	ACG	GCG	CTG	GCT	GCC	GTC	625
I	C	S	A	L	A	T	V	L	L	A	L	L	I	L	C	V	I	Y	C	193
ATC	TGC	AGT	GCT	CTG	GCC	ACG	GTG	CTG	CTC	GCC	CTG	CTC	ATC	CTG	TGT	GTC	ATC	TAC	TGC	685
K	R	Q	F	M	E	K	K	P	S	C	K	L	P	S	L	C	L	T	V	213
AAG	AGG	CAG	TTC	ATG	GAG	AAG	AAA	CCC	AGC	TGT	AAG	CTC	CCA	TCC	CTC	TGT	CTC	ACT	GTG	745
K	*																			215
AAG	TGA																			751
GCTTGTTAGCATTGTCAACCAAGAGTTCTCAAGACACCTGGCTGAGACCTAAGACCTTTAGAGCATCAACAGCTACTTA																				830
GAATACAAGATGCAGGAAAACGAGCCTCTTCAGGAATCTCAGGGCCTCCTAGGGATGCTGGCAAGGCTGTGATGTCTCA																				909
AGGCTACCAAGGAAAAAATAAAAGTTGTCTATACCCTAAAAAAAAAAAAAAAAAAAAAAAAACATGCGGCCGC																				981

Fig. 12B

```
GAATTCCGGCACGAGGGCGTTTGGCGCGGAAGTGCTACCAAGCTGCGGAAAGCGTGAGTCTGGAGCACAGCACTGGCGAG 79

                                     M  A  L  K  V  L  P  L  H  R  T  V      12
TAGCAGGAATAAACACGTTTGGTGAGAGCC ATG GCA CTC AAG GTC CTA CCT CTA CAC AGG ACG GTG 145

L  F  A  A  I  L  F  L  L  H  L  A  C  K  V  S  C  E  T  G      32
CTC TTC GCT GCC ATT CTC TTC CTA CTC CAC CTG GCA TGT AAA GTG AGT TGC GAA ACC GGA 205

D  C  R  Q  Q  E  F  K  D  R  S  G  N  C  V  L  C  K  Q  C      52
GAT TGC AGG CAG CAG GAA TTC AAG GAT CGA TCT GGA AAC TGT GTC CTC TGC AAA CAG TGC 265

G  P  G  M  E  L  S  K  E  C  G  F  G  Y  G  E  D  A  Q  C      72
GGA CCT GGC ATG GAG TTG TCC AAG GAA TGT GGC TTC GGC TAT GGG GAG GAT GCA CAG TGT 325

V  P  C  R  P  H  R  F  K  E  D  W  G  F  Q  K  C  K  P  C      92
GTG CCC TGC AGG CCG CAC CGG TTC AAG GAA GAC TGG GGT TTC CAG AAG TGT AAG CCA TGT 385

A  D  C  A  L  V  N  R  F  Q  R  A  N  C  S  H  T  S  D  A      112
GCG GAC TGT GCG CTG GTG AAC CGC TTT CAG AGG GCC AAC TGC TCA CAC ACC AGT GAT GCT 445

V  C  G  D  C  L  P  G  F  Y  R  K  T  K  L  V  G  F  Q  D      132
GTC TGC GGG GAC TGC CTG CCA GGA TTT TAC CGG AAG ACC AAA CTG GTT GGT TTT CAA GAC 505

M  E  C  V  P  C  G  D  P  P  P  P  Y  E  P  H  C  E  *      151
ATG GAG TGT GTG CCC TGC GGA GAC CCA CCT CCT CCC TAC GAA CCA CAC TGT GAG TGA 562

TGTGCCAAGTGGCAGCAGACCTTTAAAAAAAAGAAAAAAAACAAACAAAAACAAAAAAAACAAAAAAAACAAAAAAA 641

ATTTCCGCGGCCGC 655
```

Fig. 13

	MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCK	Majority
	10 20 30 40 50	
1	MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCK	muT127a
1	MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCK	muT127b
1	MYVWVQQ-----PTALLLLALTLGVTTARRLNCVKHTYPS-GHKC--CR	ox40
	QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR	Majority
	60 70 80 90 100	
51	QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR	muT127a
51	QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR	muT127b
41	ECQPGHGMVSRG--DHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNHRSG	ox40
	FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH	Majority
	110 120 130 140 150	
101	FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH	muT127a
101	FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH	muT127b
89	SELKQNCPTPTQDTVC-RCRPGTQPRQD-SGYKLGVDVPC--PPGHFSPG	ox40

Fig. 14A

22/68

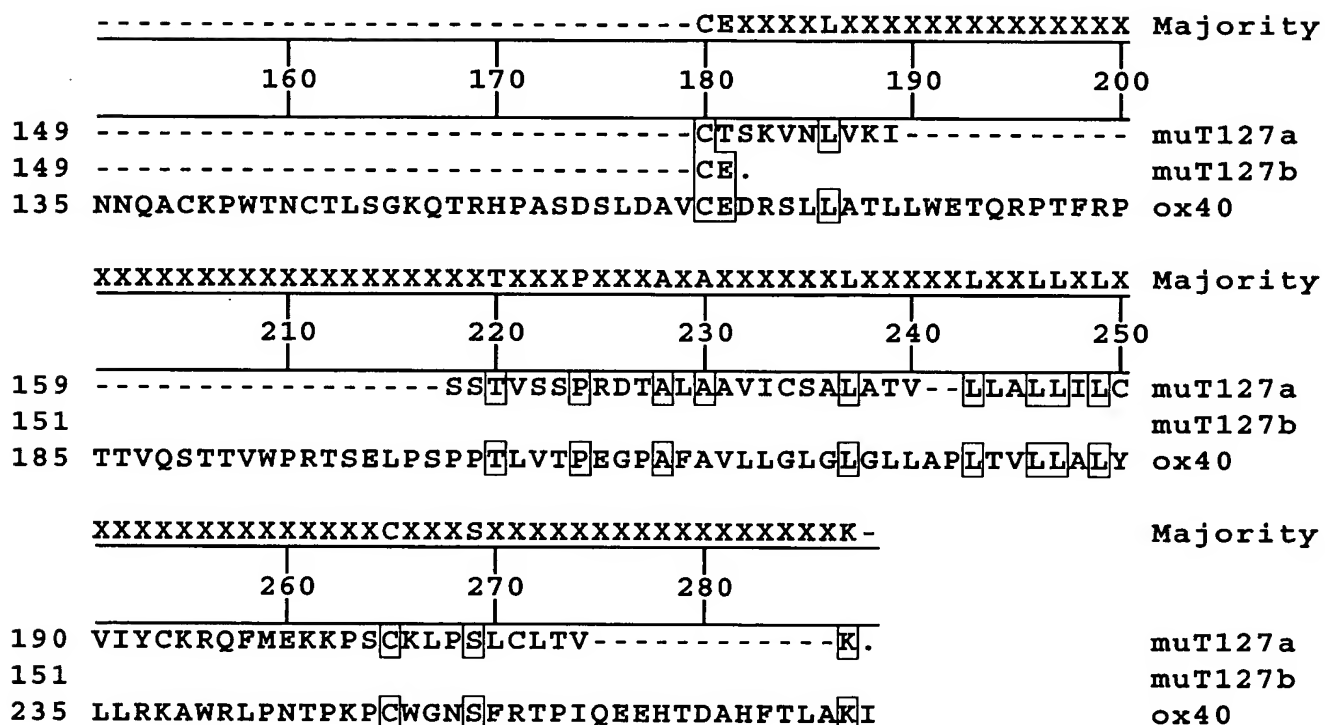


Fig. 14B

23/68

**Fig. 15A**

	70	80	90	100	110	120
T127A	ECGFGYGEDAQCVPPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG					
	::: ::: ::: :::					
	ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG					
	70	80	90	100	110	120
	130	140	150	160	170	180
T127A	FYRKTKLVGFQDMECVPCGDP PPPYEPHCTSKVNLVKISSTVSSPRDTALA AVICSALAT					
	::: ::: ::: :::					
	FYRKTKLVGFQDMECVPCGDP PPPYEPHCASKVNLVKIA STASSPRDTALA AVICSALAT					
	130	140	150	160	170	180
	190	200	210			
T127A	VLLALLILCVIYCKRQFMEKKPSCKLPSLC LTVKN					
	::: ::: ::: :X					
	VLLALLILCVIYCKRQFMEKKPSWSLSQDIQYNGSELSC LDPRQLHEYAHRACCQCRRD					
	190	200	210	220	230	240

**Fig. 15B**



25/68

FASTA searches a protein or DNA sequence data bank  
version 2.0u53 July, 1996  
Please cite:  
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

inputs/nb504897.tmp : 981 aa  
> Atm472300: 981 aa  
vs library  
searching inputs/nb658900.tmp library

1496 residues in 1 sequences  
The best scores are: initn initl opt  
Patent Nucleotide V33362 - (untitled) 2575 2575 2861  
>> Patent Nucleotide V33362 - (untitled) (1496 aa)  
initn: 2575 initl: 2575 opt: 2861  
Smith-Waterman score: 2888; 70.6% identity in 922 aa overlap

	40	50	60	70	80	90
Atm47	CCCCAGCCTCAAACCTGCAGTCCGGCGCCGCGGGGCAGGACAAGGGGAAGGAATAAACACG					
	X:..... .. : .. ::::: ...					
	GGGAACGTAGAACTCTCCAACAATAAATACA					
	10	20	30			

Fig. 16A

**Fig. 16B**

```

                220          230          240          250          260          270
Atm47 GCAGGAATTCAAGGATCGATCTGGAACTGTGTCCTCTGCAAACAGTGCGGACCTGGCAT
      ..... : ..... : ..... : ..... : ..... : ..... :
GCAAGAATTCAGGGATCGGTCTGGAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCAT
                160          170          180          190          200          210
                280          290          300          310          320          330
Atm47 GGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGCCCTGCAG
      ..... : ..... : ..... : ..... : ..... : ..... :
GGAGTTGTCTAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCG
                220          230          240          250          260          270
```

Fig. 16C

```

      340      350      360      370      380      390
Atm47 GCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTGCGGACTGTGC
      :: :::: :::::::::::::::::::::: :::::::::::::: ::::: ::: ::::: ::
      GCTGCACAGGTTCAAGGAGGACTGGGGCTTCCAGAAATGCAAGCCCTGTCTGGACTGCGC
      280      290      300      310      320      330
      400      410      420      430      440      450
Atm47 GCTGGTGAACCGCTTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTGTCTGCGGGGA
      . :::::::::::::::::::::: :: :: ::: :::::::::::::: ::::::::::::::
      AGTGGTGAACCGCTTTTCAGAAGGCAAATTGTTTCAGCCACCAGTGATGCCGTCTGCGGGGA
      340      350      360      370      380      390
```

Fig. 16D

```

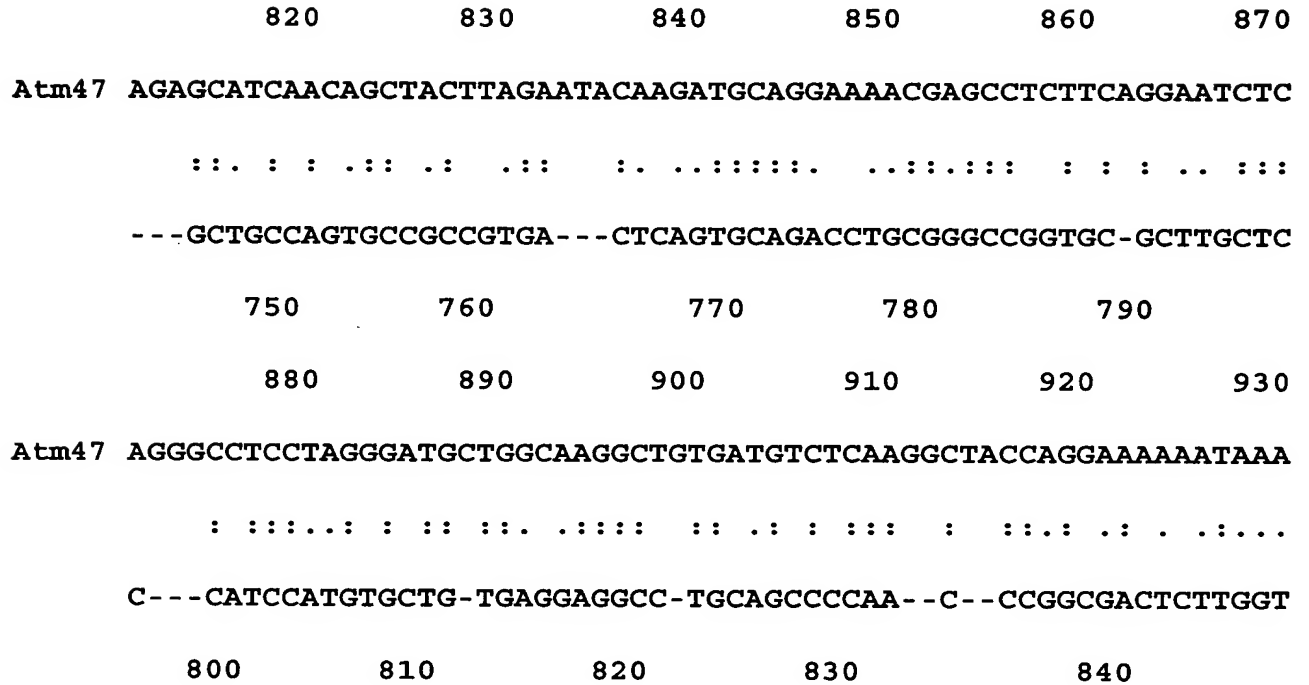
      460      470      480      490      500      510
Atm47 CTGCCTGCCAGGATTTTACCGGAAGACCAAACCTGGTTGGTTTTCAAGACATGGAGTGTGT
      :::: :::::::::::::: :::::::::: :::: :: :: ::::::::::::::::::::
      CTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGT
      400      410      420      430      440      450
      520      530      540      550      560      570
Atm47 GCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGGTGAACCTTGT
      ::: :: :::::::::::::::::::: :::::::::::::::::::: :::: ::
      GCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGT
      460      470      480      490      500      510
```

Fig. 16E

**Fig. 16F**

	700	710	720	730	740	750
Atm47	G TTCATGGAGAAGAAACCCAGCTGTAAGCTCCCATCCCTCTGTCTCACTGTGAAGTGAGC					
	::: ::::::::::::::::::::::: . :: : .:: :. .... ::. : ::					
	GTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCACA-GGACATTCAGTACAACG-GC					
	640	650	660	670	680	
	760	770	780	790	800	810
Atm47	T TGTTAGCATT-GTCACCCAAGAGTTCTCAAGACACCT-GGCTGAGACCTAAGA-CCTTT					
	: : ::. : :. :. :. :^: v. ::. :. :. :. :. :. :. :. :. :.					
	TC-TGAGCTGTCGTGTCTTGACAGACCTCAG--CTCCACGAATATGCCCACAGAGCCT--					
	690	700	710	720	730	740

Fig. 16G



**Fig. 16H**





Fig. 17

T118 pileup.msf MSF: 286

1913 ..

Name: Trash Len: 286 Check: 7625 Weight: 1.00

Name: TNF Len: 286 Check: 5421 Weight: 1.00

Name: tweak Len: 286 Check: 8867 Weight: 1.00

//

	1	60
TRASH	MPASSPFL...LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTTELQS	
TNF	MSTESMIRDVELAEALPKKTGGP...QGSRRCLFLSLFSFL.....IVAGATTLC	
tweak	MAARR.....SQRRRGRRGEPGTALLVPLALGLGL.....ALAC.LGLLLAVVSLGS	

	61	120
TRASH	LRREVSRLQ.GTGGPSQNGEGYPWQ.SLPEQSSDALEAWENGERSRKRRAVLTQKQKKQH	
TNF	L.....LHFGVIGPQR..EEFPRDLSLISPLAQAV.....RSSSRTP.....SDK	
tweak	.RASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVPRRSAPKGRKTRARR	

	121	180
TRASH	SV.....LHLVPINATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR.....IQDAGVYLL	
TNF	PV.....AHVVANPQAE.....GQLQWLN..RRANALLANGVELRDNQLVVPSEGLYLI	
tweak	AIAAHYEVHPRPGQDGAQAGVDGTVSGWEEA..RINSSSPLRYNRQIGEFIVTRAGLYYL	

	181	240
TRASH	YSQVLFQDVTFTMGQVVSREGQGRQETLFR.....CIRSMPSHPDRA....	
TNF	YSQVLFKQGQCPSTHVLLTHTISRIAVSYQTKVNLL..SAIKSPCQRETPEGAEAK..PW	
tweak	YCQVHFDEG.....KAVYL.KDLLVDGVLALRCLEEFSAATAASSLGPQ	

	241	286
TRASH	YNCSYAGVFLHQLHGDILSV.IIPRARAKLNLSPHG.TFLGFVKL.	
TNF	YEPIYLGGVFQLEKGDRLSA.EINRPDY.LDFAESGQVYFGIIAL.	
tweak	LRLCQVSGLLALRPGSSLRIRTLPAHLK...AAPFLTYFGLFQVH	

Fig. 18

36/68

GTCGACCCAC	GCGTCCGGCA	GGATGTTTGC	AGTGTGCGGC	CCAGGGCTCT	GAGACTGAGC	60
CTGCCATCCA	CTCGCACGCC	TTTCTTTTCAG	GGCTTTTCGG	CTGTTGGCTA	CACTGATGTG	120
ACCCCCCTCC	CTTTTGTGGA	ATG ATG GGG ATC TTT TTG GTG TAT GTT GGA TTT	172			
		Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe				
		1 5 10				
GTT TTC TTT TCC GTT TTA TAT GTA CAA CAA GGG CTT TCT TCT CAA GCA	220					
Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala						
	15 20 25					
AAA TTT ACC GAG TTT CCG CGG AAC GTG ACG GCG ACC GAG GGG CAG AAT	268					
Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn						
	30 35 40					
GTG GAG ATG TCC TGC GCC TTC CAG AGC GGC TCC GCC TCG GTG TAT CTG	316					
Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu						
	45 50 55					
GAG ATC CAA TGG TGG TTC CTG CGG GGG CCG GAG GAC CTG GAT CCC GGG	364					
Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly						
	60 65 70 75					
GCC GAG GGG GCC GGC GCG CAG GTG GAG CTC TTG CCC GAC AGA GAC CCG	412					
Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro						
	80 85 90					
GAC AGC GAC GGG ACC AAG ATC AGC ACA GTG AAA GTC CAA GGC AAT GAC	460					
Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp						
	95 100 105					
ATC TCC CAC AAG CTT CAG ATT TCC AAA GTG AGG AAA AAG GAT GAA GGC	508					
Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly						
	110 115 120					
TTA TAT GAG TGC AGG GTG ACT GAT GCC AAC TAC GGG GAG CTT CAG GAA	556					
Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu						
	125 130 135					
CAC AAG GCC CAG GCC TAT CTG AAA GTC AAT GCC AAC AGC CAT GCC CGC	604					
His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg						
	140 145 150 155					
AGA ATG CAG GCC TTC GAA GCC TCG CCC ATG TGG CTG CAG GAT ATG AAG	652					
Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys						
	160 165 170					
CCC CGC AAG AAC GTC TCC GCA GCC ATC CCC AGC AGC ATC CAT GGC TCT	700					
Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser						
	175 180 185					
GCC AAC CAA CGA ACG CAC TCC ACC TCC AGC CCT CAA GTG GTA GCC AAA	748					
Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val Ala Lys						
	190 195 200					

Fig. 19A

ATC CCC AAA CAA AGT CCA CAA TCA GGT ATG GAA ACC CAT TTC GAG CCT	796
Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro	
205 210 215	
TTT ATT TTA CCA CTC ACA AAC GCT CCA CAG AAA GGT CAG TCG TAT AGA	844
Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg	
220 225 230 235	
GTA GAC AGA TTT ATG AAT GGT GAT TTT TAAAATCGGA GACCTAGTTC	891
Val Asp Arg Phe Met Asn Gly Asp Phe	
240	
AGTGCAAGTG ATTATGAGAG GTGAGCACTG AGCCTGCACC AATTCACTCA GAGCTCAAAG	951
CATGTGGGTG CACCCCGTCA GTCCCCTAGT GGTGCTTCAT TTCCAGGGCA TCTGAGAGCT	1011
GGACTCTGGT TTTTATCCTT TCTGTATTTA CACATTATAA GAACAATAAA TCATGTAATG	1071
TTGGTTACAT TACAAAAAAA AAAAAAAAAA AAAAAAAGG GCGGCCGC	1119

Fig. 19B

38/68

CACGCGTCCG CAGCCAGCCG GCGGCGGAGA CACTTCACGG CGTGGCAACC CGGGTCTGTG	60
CCTTGAAGCC TCCGGATCGC AGCCAGCTCG GTCCATCCCT CACTAGTCGC AATCCCCTGT	120
GTCCAAGCTA CTCTTTGCTA TGAGCGGCAG CATGCGTGCA GTATCGCGCC CCAGGCTCTG	180
AGAGCAGCCT GCGGACACGC TTGCCTATCT GTCITTTTATAG GTTTTGGGGC TCTGGGCTAC	240
ACGGATGTGC CCCACTCCCT TGGCATG ATG GGG ATC TTT TTG GCG TCT GTT	291
Met Gly Ile Phe Leu Ala Ser Val	
1 5	
GGA TTT ATG TTC TTT TCC GTG TTA TAT GTA CAA CAA GGG CTT TCT TCT	339
Gly Phe Met Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser	
10 15 20	
CAA GCA AAA TTT ACC GAG TTG CCG AGA AAT GTG ACT GCT ACC GAA GGG	387
Gln Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly	
25 30 35 40	
CAA AAT GTG GAG ATG TCC TGT GCT TTC CAA AGC GGC TCT GCT TCA GTG	435
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val	
45 50 55	
TAC CTG GAG ATC CAG TGG TGG TTC CTT CGG GGG CCA GAG GAC CTG GAG	483
Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu	
60 65 70	
CAA GGC ACG GAG GCT GCA GGC TCG CAG GTG GAG CTC TTA CCC GAC AGA	531
Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg	
75 80 85	
GAC CCG GAC AAC GAT GGG ACC AAG ATT AGT ACA GTG AAA GTC CAA GGC	579
Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly	
90 95 100	
AAT GAT ATC TCC CAC AAG CTT CAG ATA TCC AAA GTG AGA AAA AAG GAT	627
Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp	
105 110 115 120	
GAA GGT TTA TAC GAG TGC AGG GTG ACT GAC GCT AAC TAC GGG GAG CTT	675
Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu	
125 130 135	
CAG GAA CAC AAG GCC CAG GCC TAT CTG AAA GTC AAT GCC AAC AGC CAT	723
Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His	
140 145 150	
GCT CGG AGG ATG CAG GCC TTT GAA GCC TCA CCT ATG TGG CTG CAA GAC	771
Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp	
155 160 165	
ACG AAG CCT CGA AAG AAC GCA TCA TCG GTG GTT CCC AGC AGC GTC CAC	819
Thr Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His	
170 175 180	

Fig. 20A

39/68

AAC TCT GCC AAC CAA CGA ATG CAC TCC ACC TCC AGC CCT CAA GCG GTA Asn Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val 185 190 195 200	867
GCC AAA ATC CCC AAG CAA AGT CCA CAA TCA GCA AAG AGC AAA TCG CCT Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro 205 210 215	915
GTA AAA TCT ACG GAG CGG ACA GCA AAG TTG ACC CTA TAC TCC AAG CAC Val Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His 220 225 230	963
CAT TCT GCA CCC CTG TAC TCT AGT TAT CTA CAC AAG GAG CAT CAG CTT His Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu 235 240 245	1011
CCG GAA GCA TAAGTGAAGA CACTGTCACA CGCTTTATTG ATAATATTTT Pro Glu Ala 250	1060
CTTTGGGAAG TTGCTGATCT TTTATTTCAA GAGAATTAAT GGGAAGAGAT AGGACATTTT	1120
CCAATTACAA GACCAATTTT TTTCTTTTA TTTCAACAA TAAAACCTGC ATTTCACTGA	1180
CTGCTCAGGA GTTGGCCTGA ATGACATCAG TATACTAAAT ATTTCCATGG ATTCACCAA	1240
TTTCCTAACG AGGGACACCT AATCTTCAAG AAGCAAACAA AGATGGAAAA CCTAAGAACC	1300
ACAAACTGTC TCATACAGCA CCCAGCTGA GGAACAAAAC AAATAGCTAA ATGCTGACCA	1360
TGGCAAATCA ACATCAGACA ACTTTATTTT ACATATGGAA TAATCAAAGA AAGTTTTTTT	1420
TTTACTTCCT TTTTGCCCCC TGGAATTTAT CTTGGAGTTT CCTTTTTTC CTTGATTGCC	1480
GTTTTCGTTC AATGGTAGCA AGTGCCAATT ATGGCCAATC CTTGTCAATC CTGGAAGGTT	1540
TATATTCATA TACATTGAGT GTGGTATATA TCAATGTATT TTAATTCATT TGGCAATTTT	1600
TGTATAGGCA AACCTGGCAA ATTCTGTAAA TTGCTTATAG TATGTGTGAT ATGACTTCAA	1660
GGTAGATAGG CTATGATGCT CATGCAAGCT GACTTTCTTC ATTCTATATA CAAATATATT	1720
CATGAGCATA TATTAGGCCA CCAACTTCTT TTCCTAAAGA ATTATTTTTT ATTTGTACCT	1780
CATGTATTTT GTGAATTTTG TAGTATATTT CTCTGTTCCA CTAGTTTGAC CGCTACAGTT	1840
TGTCTCTGTT GTCCTCTACT TCCTTCTGGA AAAATTTAAA ATTGTGTATG TCTCTGATAA	1900
ATGAATTAAT TTTGTTGTGT GTATGCTATG TTGGAATTTG CTGTGTTCTT TTAAACATGT	1960
ATTTATTAAG GTTTGGGGAT CTTGAGTTGA GTCTGAAGAA TGCACACCTG GTTTTTGACA	2020
GAGTTCCTCA TGTTACCAAT ATTCTATCTC AGAGAAAGAA AGACACCAAG TGGGAAAAC	2080
AAGAAGACAT TTTGACTTCC CAAGATCCTG GAAGAGCACT TCACACTCTG ACTAAATAAT	2140
GTTGCTTTTT TTGTTCTTCA AGACTTTTTT GTAGCTTTGT CTTTCTGTTA GTTGCTGCTA	2200
ATTATATTTT AATGTCTACT AATTAAAAAT TAAAATGTGA TTGTTGGCTG AATACAATAT	2260

Fig. 20B

GCAAATGACT GCAAAGCCCA TACTGAAGAA AATAGATGTT TAATCTTCAC TCAATAATTA	2320
TAATTTTAAA TAGTTCATCA TTATTTTTTG ACCTTATGAT ATTTTGTTTA GACCTGTTCT	2380
AATTACATCT TTCTCTGGCA AAGAAAGATA GAACAATCAA TACATTCCCT CTTACAGTAT	2440
GGAATGGTTG TGGCTTAAGA AAGAATGCAT CCAGATGGTC TTCCAGAGAG ATTATTTTAT	2500
TTTCATTATA AAACCAGAAA CCATATATGT AGGAATGGTT CATTCTAAT GTAAGGCCAT	2560
AAATTGTAGC TTGAAGGCAA GGAATACATT TGTTTTTTTA TGGTAAAGGA CTGGCCTCTG	2620
ACATGCACTT ATAAGCAATG TGAATATTTT CATAATATGC TTGACATTCT CCTTTAACAA	2680
ATATTGTTTT ATGGTAAATC TTTCTTGCC ATTTTCTTC TTTCATTGA TTCATTATTT	2740
CATTCTAATG AAGAAAATAA AGGTTTAATT ATGATACTTT ATTAACATAC AAATGTATTT	2800
TCTTTCTAAG TTAAATATCT GAAAGTTGTA TAAATGATG GTAGAGAAAT ATTACTCATT	2860
CGGTTTCTTT GAGCTTTAAG AATCCCATAC ATTGCAGTAT ATATTAGAAT ACTGATTTAA	2920
CATCAAACCTG GGGGGGAAAA TCATGTATTA TACTTTTACT CAATGTCTAG GTAATGGATT	2980
CAGCTAATTT TACAGCAAGC CAAATGTGTA CCCGTATCAG TAATGTTTAC CATGCTTGTA	3040
ATAAAAGGGC ATATGCTAGT TTTGGAAGAA TGCTCATTAG ATTCATTGTA TCAGTGTCCA	3100
AAATAATAAA GACCTGTTTA TCACTGTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3160
AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC GGCCGC	3196

Fig. 20C



Elapsed time: 0:00:00

Fig. 21

GTCGACCCACGCGTCCGGAGCCCGGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGG	79
GCCCGACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCCGCGCCTCCCGGGACAGAA	158
M C S R V P L L L P L L L L A L G P	19
G ATG TGC TCC AGG GTC CCT CTG CTG CTG CCG CTG CTC CTG CTA CTG GCC CTG GGG CCT	216
G V Q G C P S G C Q C S Q P Q T V F C T	39
GGG GTG CAG GGC TGC CCA TCC GGC TGC CAG TGC AGC CAG CCA CAG ACA GTC TTC TGC ACT	276
A R Q G T T V P R D V P P D T V G L Y V	59
GCC CGC CAG GGG ACC ACG GTG CCC CGA GAC GTG CCA CCC GAC ACG GTG GGG CTG TAC GTC	336
F E N G I T M L D A G S F A G L P G L Q	79
TTT GAG AAC GGC ATC ACC ATG CTC GAC GCA GGC AGC TTT GCC GGC CTG CCG GGC CTG CAG	396
L L D L S Q N Q I A S L P S G V F Q P L	99
CTC CTG GAC CTG TCA CAG AAC CAG ATC GCC AGC CTG CCC AGC GGG GTC TTC CAG CCA CTC	456
A N L S N L D L T A N R L H E I T N E T	119
GCC AAC CTC AGC AAC CTG GAC CTG ACG GCC AAC AGG CTG CAT GAA ATC ACC AAT GAG ACC	516
F R G L R R L E R L Y L G K N R I R H I	139
TTC CGT GGC CTG CGG CGC CTC GAG CGC CTC TAC CTG GGC AAG AAC CGC ATC CGC CAC ATC	576

Fig. 22A

Q	P	G	A	F	D	T	L	D	R	L	L	E	L	K	L	Q	D	N	E	159
CAG	CCT	GGT	GCC	TTC	GAC	ACG	CTC	GAC	CGC	CTC	CTG	GAG	CTC	AAG	CTG	CAG	GAC	AAC	GAG	636
L	R	A	L	P	P	L	R	L	P	R	L	L	L	L	D	L	S	H	N	179
CTG	CGG	GCA	CTG	CCC	CCG	CTG	CGC	CTG	CCC	CGC	CTG	CTG	CTG	CTG	GAC	CTC	AGC	CAC	AAC	696
S	L	L	A	L	E	P	G	I	L	D	T	A	N	V	E	A	L	R	L	199
AGC	CTC	CTG	GCC	CTG	GAG	CCC	GGC	ATC	CTG	GAC	ACT	GCC	AAC	GTG	GAG	GCG	CTG	CGG	CTG	756
A	G	L	G	L	Q	Q	L	D	E	G	L	F	S	R	L	R	N	L	H	219
GCT	GGT	CTG	GGG	CTG	CAG	CAG	CTG	GAC	GAG	GGG	CTC	TTC	AGC	CGC	TTG	CGC	AAC	CTC	CAC	816
D	L	D	V	S	D	N	Q	L	E	R	V	P	P	V	I	R	G	L	R	239
GAC	CTG	GAT	GTG	TCC	GAC	AAC	CAG	CTG	GAG	CGA	GTG	CCA	CCT	GTG	ATC	CGA	GGC	CTC	CGG	876
G	L	T	R	L	R	L	A	G	N	T	R	I	A	Q	L	R	P	E	D	259
GGC	CTG	ACG	CGC	CTG	CGG	CTG	GCC	GGC	AAC	ACC	CGC	ATT	GCC	CAG	CTG	CGG	CCC	GAG	GAC	936
L	A	G	L	A	A	L	Q	E	L	D	V	S	N	L	S	L	Q	A	L	279
CTG	GCC	GGC	CTG	GCT	GCC	CTG	CAG	GAG	CTG	GAT	GTG	AGC	AAC	CTA	AGC	CTG	CAG	GCC	CTG	996
P	G	D	L	S	G	L	F	P	R	L	R	L	L	A	A	A	R	N	P	299
CCT	GGC	GAC	CTC	TGG	GGC	CTC	TTC	CCC	CGC	CTG	CGG	CTG	CTG	GCA	GCT	GCC	CGC	AAC	CCC	1056
F	N	C	V	C	P	L	S	W	F	G	P	W	V	R	E	S	H	V	T	319
TTC	AAC	TGC	GTG	TGC	CCC	CTG	AGC	TGG	TTT	GGC	CCC	TGG	GTG	CGC	GAG	AGC	CAC	GTC	ACA	1116

Fig. 22B

L	A	S	P	E	E	T	R	C	H	F	P	P	K	N	A	G	R	L	L	339
CTG	GCC	AGC	CCT	GAG	GAG	ACG	CGC	TGC	CAC	TTC	CCG	CCC	AAG	AAC	GCT	GGC	CGG	CTG	CTC	1176
L	E	L	D	Y	A	D	F	G	C	P	A	T	T	T	T	A	T	V	P	359
CTG	GAG	CTT	GAC	TAC	GCC	GAC	TTT	GGC	TGC	CCA	GCC	ACC	ACC	ACC	ACA	GCC	ACA	GTG	CCC	1236
T	T	R	P	V	V	R	E	P	T	A	L	S	S	S	L	A	P	T	W	379
ACC	ACG	AGG	CCC	GTG	GTG	CGG	GAG	CCC	ACA	GCC	TTG	TCT	TCT	AGC	TTG	GCT	CCT	ACC	TGG	1296
L	S	P	T	A	P	A	T	E	A	P	S	P	P	S	T	A	P	P	T	399
CTT	AGC	CCC	ACA	GCG	CCG	GCC	ACT	GAG	GCC	CCC	AGC	CCG	CCC	TCC	ACT	GCC	CCA	CCG	ACT	1356
V	G	P	V	P	Q	P	Q	D	C	P	P	S	T	C	L	N	G	G	T	419
GTA	GGG	CCT	GTC	CCC	CAG	CCC	CAG	GAC	TGC	CCA	CCG	TCC	ACC	TGC	CTC	AAT	GGG	GGC	ACA	1416
C	H	L	G	T	R	H	H	L	A	C	L	C	P	E	G	F	T	G	L	439
TGC	CAC	CTG	GGG	ACA	CGG	CAC	CAC	CTG	GCG	TGC	TTG	TGC	CCC	GAA	GGC	TTC	ACG	GGC	CTG	1476
Y	C	E	S	Q	M	G	Q	G	T	R	P	S	P	T	P	V	T	P	R	459
TAC	TGT	GAG	AGC	CAG	ATG	GGG	CAG	GGG	ACA	CGG	CCC	AGC	CCT	ACA	CCA	GTC	ACG	CCG	AGG	1536
P	P	R	S	L	T	L	G	I	E	P	V	S	P	T	S	L	R	V	G	479
CCA	CCA	CGG	TCC	CTG	ACC	CTG	GGC	ATC	GAG	CCG	GTG	AGC	CCC	ACC	TCC	CTG	CGC	GTG	GGG	1596
L	Q	R	Y	L	Q	G	S	S	V	Q	L	R	S	L	R	L	T	Y	R	499
CTG	CAG	CGC	TAC	CTC	CAG	GGG	AGC	TCC	GTG	CAG	CTC	AGG	AGC	CTC	CGT	CTC	ACC	TAT	CGC	1656

Fig. 22C

N	L	S	G	P	D	K	R	L	V	T	L	R	L	P	A	S	L	A	E	519
AAC	CTA	TCG	GGC	CCT	GAT	AAG	CGG	CTG	GTG	ACG	CTG	CGA	CTG	CCT	GCC	TCG	CTC	GCT	GAG	1716
Y	T	V	T	Q	L	R	P	N	A	T	Y	S	V	C	V	M	P	L	G	539
TAC	ACG	GTC	ACC	CAG	CTG	CGG	CCC	AAC	GCC	ACT	TAC	TCC	GTC	TGT	GTC	ATG	CCT	TTG	GGG	1776
P	G	R	V	P	E	G	E	E	A	C	G	E	A	H	T	P	P	A	V	559
CCC	GGG	CGG	GTG	COG	GAG	GGC	GAG	GAG	GCC	TGC	GGG	GAG	GCC	CAT	ACA	CCC	CCA	GCC	GTC	1836
H	S	N	H	A	P	V	T	Q	A	R	E	G	N	L	P	L	L	I	A	579
CAC	TCC	AAC	CAC	GCC	CCA	GTC	ACC	CAG	GCC	CGC	GAG	GGC	AAC	CTG	CCG	CTC	CTC	ATT	GCG	1896
P	A	L	A	A	V	L	L	A	A	L	A	A	V	G	A	A	Y	C	V	599
CCC	GCC	CTG	GCC	GCG	GTG	CTC	CTG	GCC	GCG	CTG	GCT	GCG	GTG	GGG	GCA	GCC	TAC	TGT	GTG	1956
R	R	G	R	A	M	A	A	A	A	Q	D	K	G	Q	V	G	P	G	A	619
CGG	CGG	GGG	CGG	GCC	ATG	GCA	GCA	GCG	GCT	CAG	GAC	AAA	GGG	CAG	GTG	GGG	CCA	GGG	GCT	2016
G	P	L	E	L	E	G	V	K	V	P	L	E	P	G	P	K	A	T	E	639
GGG	CCC	CTG	GAA	CTG	GAG	GGA	GTG	AAG	GTC	CCC	TTG	GAG	CCA	GGC	CCG	AAG	GCA	ACA	GAG	2076
G	G	G	E	A	L	P	S	G	S	E	C	E	V	P	L	M	G	F	P	659
GGC	GGT	GGA	GAG	GCC	CTG	CCC	AGC	GGG	TCT	GAG	TGT	GAG	GTG	CCA	CTC	ATG	GGC	TTC	CCA	2136
G	P	G	L	Q	S	P	L	H	A	K	P	Y	I	*						674
GGG	CCT	GGC	CTC	CAG	TCA	CCC	CTC	CAC	GCA	AAG	CCC	TAC	ATC	TAA						2181

Fig. 22D

GCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTA 2260  
AGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCG 2339  
GTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT 2418  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGC 2497  
TGGGCTCTCCCACTCCAGGCGGACCCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCG 2576  
GCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTT 2655  
TGCTTTTTTAAAATATATATATATTTATAAGAGATCCTTTCCATTTATTTCTGGGAAGATGTTTTTCAAACCTCAGAGAC 2734  
AAGGACTTTGGTTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAGAAAAAATAAAAGATGAAGTGTGAAAAAA 2813  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2852

Fig. 22E

	1	60
LRSG-1	MCSRVP LLLPL LLLL ---ALGP-GVQG-----CPSGCQCS-----QPQTVFC	
GPV	M-LRGTLLCAVLGLLR-----AQPFPCPPACKCVFRDAAQ-----C	
IGFBP	MALRKGG LALALL LLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACS YDDEVNELSVFC	
	61	120
LRSG-1	TARQGTTVPR-DVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQ	
GPV	SGGDVARISALGLP-----TNLTHILLFGMGRGV LQSQSFS	
IGFBP	SSRNLTRLPD-GIPGGTQALWLD SNNLSSIPPAAFRNLS SLAFLNLQGGQLGSLEPQALL	
	121	180
LRSG-1	PLANLSNLDLTANRLHEITNETFRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLLELKLQD	
GPV	GMTVLQRLMISDSHISAVAPGTFSDLIKLKT LRLSRNKITHLPGALLDKMVLLEQLFLDH	
IGFBP	GLENLCHLHLERNQLRSLAVGTFA YTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW	
	181	240
LRSG-1	NELRALPPLRLPRL LLLD---LSHNSLLALEPGILDT-ANVEALRLAGLGLQQLDEGLFS	
GPV	NALRGIDQNMFQKLVNLQELALNQQLDFLPASLFTNLENLKL LLDLSGNNLTHLPKGLLG	
IGFBP	NSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFA	
	241	300
LRSG-1	RLRNLHDL DVSDNQLERVPP-VIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS	
GPV	AQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFH-RNHIRSIAPGAFDRLPNLSSLTLS	
IGFBP	QLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLS-HNRVAGLLEDTFPGLLG LRVLRLS	
	301	360
LRSG-1	NLSLQALPGDLSGLFPRLRL LAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPF	
GPV	RNHLAFLPSALFLHSHNLTLLTLFENPLAEL-PGVLF GEMGGLQELWL-----NRTQL--	
IGFBP	HNAIASLRPRTFEDLHFLEELQLGHNRI RQL-AERSFEGLGQLEVLTL-----DHNQLQE	

Fig. 23A

	361		420
LRSG-1	KNAGRLL--LELDYADFG--CPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTA-PAT		
GPV	-----RTLPAAAFRLNSRLRYLGVTLSPRLSA--LPQGAFOGL		
IGFBP	VKVGAFGLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLE-GSCLGR--IRPHTFAGL		
	421	* * *	* * *480
LRSG-1	EAPSPPTAPPTVGPVPQPDCCPSTCLNGGTCHLG---TRHHLACLCPEGFTGLYCES-		
GPV	GELQVLALHSNGLTALPDGL-----LRGLGKLRRQVSLRRNRLRALPRALFRNLSSLES		
IGFBP	SGLRRLFLKDNGLVGIEEQS-----LWGLAELLELDLTSNQLTHLPHQLFQGLGKLEY		
	481		540
LRSG-1	-QMGQGTRPS-PTPVTPRPPRSLTLGIEPVSPTSRLRVGLQRYLQGS SVQLRSLRLTYRNL		
GPV	VQLDHNQLETLPGDVFGALPRLTEVLLGHNSWRCDG-LGPFLG-----WLR-QHLGL		
IGFBP	LLLSHNRLAELPADALGPLQRAFWLDVSHNRLEALPGSLLASLG-----RLR--YLN		
	541		600
LRSG-1	SGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHS		
GPV	VGGEPPRCAG-PGAHAGLPLWALPGGD--AECGPRGPPPRPAADSSSEAPVHPALAPN		
IGFBP	R--NNSLRTFT-PQPPGLERLW-LEGNP--WDCSCPLKALRDFALQNPSAVPR-----		
	601		660
LRSG-1	NHAP-----VTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV		
GPV	SSEPWWAQPVTTGKGQDHSFPGFYFLLAVQAMITVIIVFAMIK-----		
IGFBP	-----FVQAICEG-DDCQPPVYTYNNITCASPPEVAGLDL-----		
	661		718
LRSG-1	GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI		
GPV	---IGQLFRKLIRER-ALG-----		
IGFBP	-----RDLGEAHFAPC-----		

Fig. 23B



GTCGACCCACGCGTCCGGGAGCCGGAGCCAGAGACCGGGGCTGGGAAACCCAGCCCGGGACGGGACGCAGCAGCCTCT	79
GGATCCCGGGACCCCGGACCTCTCAGGACCGGCCAGAGGTGAAGGACTGAGGCCCACTGAGGCCTTGGACCGCACCGC	158
	M H S R S C L P P L 10
CTGGCTCCTTCAGCCGCAGTCGTCTCCTGGGACAGAAG ATG CAC TCC AGG AGC TGC CTG CCA CCT CTC	226
L L L L L V L L G S G V Q G C P S G C Q	30
CTG TTG TTG CTT CTG GTG CTC CTG GGG TCT GGA GTA CAG GGT TGC CCA TCA GGC TGC CAG	286
C N Q P Q T V F C T A R Q G T T V P R D	50
TGC AAC CAG CCA CAG ACA GTC TTC TGC ACT GCC CGT CAG GGA ACC ACA GTG CCC CGA GAC	346
V P P D T V G L Y I F E N G I T T L D V	70
GTG CCA CCT GAC ACA GTG GGC CTG TAC ATC TTT GAG AAC GGC ATC ACG ACA CTT GAT GTG	406
G C F A G L P G L Q L L D L S Q N Q I T	90
GGC TGT TTT GCT GGC CTT CCG GGC CTG CAG CTT CTG GAC TTG TCA CAG AAC CAG ATC ACT	466
S L P G G I F Q P L V N L S N L D L T A	110
AGC CTG CCC GGG GGC ATC TTT CAG CCA CTT GTT AAC CTC AGT AAC CTG GAC CTG ACT GCC	526
N K L H E I S N E T F R G L R R L E R L	130
AAC AAA CTG CAC GAG ATC TCC AAC GAG ACC TTC CGT GGC CTG CGG CGC CTG GAG CGC CTC	586
Y L G K N R I R H I Q P G A F D A L D R	150
TAC CTG GGC AAG AAC CGA ATT CGC CAC ATC CAA CCG GGT GCC TTC GAC GCG CTT GAT CGC	646

Fig. 24A

L	L	E	L	K	L	P	D	N	E	L	R	V	L	P	P	L	H	L	P	170
CTC	CTG	GAG	CTC	AAG	CTG	CCA	GAC	AAT	GAG	CTT	CGG	GTG	TTG	CCC	CCA	TTG	CAC	TTG	CCC	706
R	L	L	L	L	D	L	S	H	N	S	I	P	A	L	E	A	G	I	L	190
CGC	CTG	CTG	CTG	CTT	GAC	CTC	AGC	CAC	AAC	AGC	ATC	CCA	GCC	CTG	GAA	GCC	GGA	ATA	CTG	766
D	T	A	N	V	E	A	L	R	L	A	G	L	G	L	R	Q	L	D	E	210
GAT	ACC	GCC	AAT	GTA	GAG	GCA	TTG	AGG	TTG	GCT	GGC	CTA	GGG	CTG	CGG	CAG	CTG	GAT	GAG	826
G	L	F	G	R	L	L	N	L	H	D	L	D	V	S	D	N	Q	L	E	230
GGG	CTT	TTT	GGC	CGC	CTT	CTC	AAC	CTC	CAT	GAC	TTG	GAT	GTT	TCT	GAC	AAC	CAG	TTG	GAG	886
H	M	P	S	V	I	Q	G	L	R	G	L	T	R	L	R	L	A	G	N	250
CAT	ATG	CCA	TCT	GTG	ATT	CAA	GGC	CTG	CGT	GGC	CTG	ACA	CGC	CTG	CGG	CTG	GCT	GGC	AAC	946
T	R	I	A	Q	I	R	P	E	D	L	A	G	L	T	A	L	Q	E	L	270
ACC	CGT	ATT	GCC	CAG	ATA	CGG	CCC	GAG	GAC	CTC	GCT	GGT	CTG	ACT	GCC	CTA	CAG	GAA	TTG	1006
D	V	S	N	L	S	L	Q	A	L	P	S	D	L	S	S	L	F	P	R	290
GAT	GTG	AGC	AAC	CTA	AGC	CTG	CAG	GCC	CTG	CCC	AGT	GAC	CTC	TGG	AGT	CTC	TTT	CCC	CGC	1066
L	R	L	L	A	A	A	R	N	P	F	N	C	L	C	P	L	S	W	F	310
CTG	CGC	CTC	TTA	GCA	GCT	GCC	AGG	AAC	CCC	TTC	AAC	TGC	TTG	TGC	CCC	TTG	AGC	TGG	TTT	1126
G	P	W	V	R	E	N	H	V	V	L	A	S	P	E	E	T	R	C	H	330
GGT	CCT	TGG	GTG	CGT	GAG	AAC	CAT	GTT	GTG	TTG	GCC	AGC	CCT	GAG	GAG	ACG	CGT	TGT	CAC	1186

Fig. 24B

51/68

F	P	P	K	N	A	G	R	L	L	L	D	L	D	Y	A	D	F	G	C	350
TTT	CCA	CCC	AAG	AAT	GCT	GGC	CGA	CTG	CTC	CTG	GAT	CTG	GAT	TAT	GCA	GAT	TTT	GGC	TGC	1246
P	V	T	T	T	T	A	T	V	P	T	I	R	S	T	I	R	E	P	T	370
CCA	GTC	ACC	ACT	ACC	ACG	GCC	ACA	GTA	CCT	ACT	ATA	AGG	TCT	ACT	ATC	AGG	GAA	CCC	ACA	1306
L	S	T	S	S	Q	A	P	T	W	P	S	L	T	E	P	T	T	Q	A	390
CTT	TCA	ACT	TCT	AGC	CAA	GCT	CCC	ACC	TGG	CCC	AGC	CTC	ACA	GAG	CCA	ACT	ACC	CAG	GCC	1366
S	T	V	L	S	T	A	P	P	T	M	R	P	A	P	Q	P	Q	D	C	410
TCC	ACC	GTA	CTA	TCG	ACT	GCC	CCA	CCA	ACC	ATG	AGG	CCA	GCT	CCT	CAG	CCC	CAG	GAC	TGT	1426
P	A	S	I	C	L	N	G	G	S	C	R	L	G	A	R	H	H	W	E	430
CCA	GCA	TCC	ATC	TGC	CTG	AAT	GGT	GGT	AGC	TGC	CGT	TTG	GGA	GCA	AGA	CAC	CAC	TGG	GAG	1486
C	L	C	P	E	G	F	I	G	L	Y	C	E	S	P	V	E	Q	G	M	450
TGC	CTA	TGC	CCT	GAG	GGC	TTC	ATT	GGC	CTG	TAC	TGT	GAG	AGT	CCA	GTG	GAG	CAA	GGG	ATG	1546
K	P	S	S	I	P	D	T	P	R	P	P	P	L	L	P	L	S	I	E	470
AAG	CCC	AGC	TCC	ATA	CCA	GAC	ACT	CCA	AGG	CCC	CCT	CCA	CTG	CTG	CCT	CTC	AGC	ATT	GAG	1606
P	V	S	P	T	S	L	R	V	K	L	Q	R	Y	L	Q	G	N	T	V	490
CCG	GTG	AGC	CCC	ACC	TCC	TTG	CGT	GTG	AAG	CTG	CAG	CGC	TAC	TTG	CAG	GGT	AAC	ACT	GTG	1666
Q	L	R	S	L	R	L	T	Y	R	N	L	S	G	P	D	K	R	L	V	510
CAG	CTA	CGG	AGC	CTC	CGG	CTC	ACC	TAT	CGC	AAC	CTG	TCT	GGC	CCT	GAC	AAA	CGA	CTG	GTG	1726

Fig. 24C

T	L	R	L	P	A	S	L	A	E	Y	T	V	T	Q	L	R	P	N	A	530
ACA	TTA	CGG	CTG	CCT	GCT	TCA	CTT	GCA	GAG	TAT	ACA	GTC	ACC	CAG	CTG	CGA	CCC	AAT	GCC	1786
T	Y	S	I	C	V	T	P	L	G	A	G	R	T	P	E	G	E	E	A	550
ACC	TAT	TCT	ATC	TGT	GTC	ACA	CCC	TTG	GGA	GCT	GGA	CGG	ACA	CCT	GAA	GGT	GAG	GAG	GCC	1846
C	G	E	A	N	T	S	Q	A	V	R	S	N	H	A	P	V	T	Q	A	570
TGT	GGG	GAG	GCC	AAC	ACT	TCC	CAG	GCA	GTC	CGC	TCT	AAC	CAT	GCC	CCA	GTT	ACC	CAG	GCC	1906
R	E	G	N	L	P	L	L	I	A	P	A	L	A	A	V	L	L	A	V	590
CGT	GAG	GGC	AAC	CTG	CCA	CTC	CTC	ATT	GCG	CCT	GCC	CTG	GCT	GCT	GTA	CTT	CTG	GCT	GTG	1966
L	A	A	A	G	A	A	Y	C	V	R	R	A	R	A	T	S	T	A	Q	610
TTA	GCC	GCT	GCA	GGG	GCA	GCC	TAC	TGT	GTG	CGG	CGG	GCA	CGG	GCA	ACT	TCT	ACA	GCT	CAG	2026
D	K	G	Q	V	G	P	G	T	G	P	L	E	L	E	G	V	K	A	P	630
GAC	AAA	GGG	CAG	GTG	GGG	CCA	GGG	ACT	GGA	CCC	CTG	GAA	CTA	GAG	GGG	GTG	AAA	GCC	CCT	2086
L	E	P	G	S	K	A	T	E	G	G	G	E	A	L	S	G	G	P	E	650
TTG	GAG	CCA	GGC	TCC	AAG	GCA	ACA	GAG	GGA	GGT	GGG	GAG	GCT	TTG	TCA	GGT	GGT	CCT	GAA	2146
C	E	V	P	L	M	G	Y	P	G	P	S	L	Q	G	V	L	P	A	K	670
TGT	GAG	GTG	CCT	CTT	ATG	GGC	TAC	CCA	GGG	CCC	AGC	CTT	CAG	GGG	GTC	CTC	CCT	GCT	AAG	2206
H	Y	I	*																	674
CAC	TAC	ATT	TAG																	2218

Fig. 24D

ACTGGTGAGAAAGAGCAGCCAGGGGGTCAGGCTTTTCAGTCACCCACCTCCTGCTGCCACAGAAGGAAGTTCTCAGTATA 2297  
CACCACAGTGCACGTGCATGATGGAGCTGTGGGACCCTCTCTGGGCTGGGTCTCATCTGTAAGCTGCTACAGCCCAGAT 2376  
GAACTCTGCCAGCCGCCAGTGCATCCAGTACAGCGCCTGCCATCTTGTGCAATGTGCAACCTGGGATGTGAGCCCTGC 2455  
CATGTGCTGGTAACATGGCTAGGCATGTTGGGCTTCCCAAACCATGGAGTCTGGTAACCAAGTGAAGGAAGCCCCAGAA 2534  
ATAATGAGTGGGGAAGGTACTAGGGCACTGGCCTTGGCCTCAAAAGTGCAGGCACACTTGAAACTGGAAAGGAAGGTGC 2613  
TCTGGGCACATGIGGATTTGCTTCTATTGTTTTGTTTTGTTTTTCTAATGTATTTATAAAAGATCTTTTCCCATTAT 2692  
GCTGGGAAAGTGTMTTCAAACCTCAGTGACAAGGACTTTGGTMTTGTAAAGACTGTTGATGATATGAAGGCCTTTTGTA 2771  
AGAAAATAAAAAATAAAGTAAAAAAAAAAAAAAAAAGGGCGGCCGC 2815

Fig. 24E

**Fig. 25A**

55/68

```

      300      310      320      330      340      350
inputs FNCVCPLSWFGPWWRESHVTLASPEETRCHFPKKNAGRLLLELDYADFGCPATTTTATVP
      .....
      FNCLCPLSWFGPWWRENHVVLASPEETRCHFPKKNAGRLLLDLDYADFGCPVTTTTATVP
            310            320            330            340            350            360

      360      370      380      390      400      410
inputs TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGT
      .....
      TIRSTIREPTLSTSSQAPTWPSTLPTTQASTVLSTAPPTMRPAPQPQDCPASICLNNGGS
            370            380            390            400            410            420

      420      430      440      450      460      470
inputs CHLGTRHHLACLCEGFTGLYCESQMGQGTTPVTPRPPRSLTLGIEPVSPTSLRVG
      .....
      CRLGARHHWECLCEGFIGLYCESPVEQGMKPSSIPDTPRPPPLPLSLIEPVSPTSLRVK
            430            440            450            460            470            480

      480      490      500      510      520      530
inputs LQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLG
      .....
      LQRYLQGNTVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLG
            490            500            510            520            530            540

      540      550      560      570      580      590
inputs PGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCV
      .....
      AGRTPEGEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCV
            550            560            570            580            590            600
```

Fig. 25B





57/68

	1	60
human LRSG-1	MCSR---VPLLLPLLLLLLALGP-GVQG-----CPSGCQCS-----QPQTVFC	
murine LRSG-1	MHSRSC-LPPLL-LLLLVLGSG-GVQG-----CPSGCQCN-----QPQTVFC	
GPV	N-LRGITLLCAVLGLLR-----AQPFPCPPACKCVFRDAAQ-----C	
IGFBP	MALRKGGALALALLLLSWVALGPRSLGAEPGTPGEAEGPACPATCACSYDDEVNELSVFC	
	61	120
human LRSG-1	TARQGTTVPR-DVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQ	
murine LRSG-1	TARQGTTVPR-DVPPDTVGLYIFENGITTLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQ	
GPV	SGGDVARISALGLP-----TNLTHILLFGMGRGVLSQSFS	
IGFBP	SSRNLTRLPD-GIPGGTQALWLDSSNNLSSIPPAAFRNLSSLAFTNLQGGQLGSLEPQALL	
	121	180
human LRSG- 1	PLANLSNLDLTANRLHEITNETFRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQD	
murine LRSG-1	PLVNLSNLDLTANKLHEISNETFRGLRRLERLYLGKNRIRHIQPGAFDALDRLLELKLDP	
GPV	GMTVLQRLMISDSHISAVAPGTFSDLIKLTLRLSRNKITHLPGALLDKMVLLEQLFLDH	
IGFBP	GLENLCHLHLERNQLRSLAVGTFAITPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW	
	181	240
human LRSG-1	NELRALPPLRLPRLLLLD---LSHNSLLALEPGIILDT-ANVEALRLAGLGLQQLDEGLFS	
murine LRSG-1	NELRVLPPLHLPRLLLLD---LSHNSIPALEAGIILDT-ANVEALRLAGLGLRQLDEGLFG	
GPV	NALRGIDQNMFOQLVNLQELALNQQLDFLPASLFTNLENLKLDDLSGNNLTHLPKGLLG	
IGFBP	NSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFA	
	241	300
human LRSG-1	RLRNLHDLVDSDNQLELV-PPVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS	
murine LRSG-1	RLNLHDLVDSDNQLEHM-PSVIQGLRGLTRLRLAGNTRIAQIRPEDLAGLTALQELDVS	
GPV	AQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFH-RNHIRSIAPGAFDRLPNLSSLTSL	
IGFBP	QLPRLQKLYLDRNLAAVAPGAFLGLKALRWLDLS-HNRVAGLLEDTFPGLLGLRVLRLS	

Fig. 26A

58/68

	301		360
human LRSG-1	NLSLQALPGDLSGLFPRLRLAAARNPFNCVCLSWFGPWVRESHVTLASPEETRCHFPF		
murine LRSG-1	NLSLQALPSDLSSLFPRLRLAAARNPFNCLCPLSWFGPWVRENHVVLASPEETRCHFPF		
GPV	RNHLAFLPSALFLHSHNLTLLTLFENPLAEL-PGVLFGEIMGGLQELWLNRTQ-----		
IGFBP	HNAIASLRPRTFEDLHFLEELQLGHNRIQL-AERSFEGLGQLEVLTLDHNQ-----		
	361		420
human LRSG-1	KNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSP		
murine LRSG-1	KNAGRLLLDLDYADFGCPVTTTTATVPTIRSTIREPTLSTSSQAPTWPSLTEPTTQASTV		
GPV	-----L-----RT-----LPAAAFRNLSR		
IGFBP	-----LQEVKVGAF--LGLTNVAVMNLSGNCLRN-----LPEQVFRGLGK		
	421	* * *	480
human LRSG-1	PSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQGTSPS		
murine LRSG-1	LSTAPPTMRPAPQPQDCPASICLNGGSCRLGARHHWECLCEGFIGLYCESPVEQGMKPS		
GPV	LRYLGVTLSP-----RLSA-----LPQGAFQGL-----		
IGFBP	LHSLHLE-GS-----CLGR-----IRPHTFAGL-----		
	481		540
human LRSG-1	PTPVTPRPSPSLTLGIEPVSPTSLRVGLQRYLQGS--SVQLRSL-RLTYRNLSGPDKRLV		
murine LRSG-1	SIPDTPRPPPLPLSIEPVSPTSLRVKLQRYLQGN--TVQLRSL-RLTYRNLSGPDKRLV		
GPV	---GELQVLALHSNGLTALPDGLLR-GLGKLQVSLRRNRLRALPRALFRNLSSLESVQL		
IGFBP	---SGLRRLFLKDNGLVGIEEQSLW-GLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLL		
	541		600
human LRSG-1	TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQA		
murine LRSG-1	TLRLPASLAEYTVTQLRPNATYSICVTPLGAGRTPEGEEACGEANTSQAVRSNHAPVTQA		
GPV	DHNQLETLPGDVFGALPRLTEVLLGHNSW-----RCDG-LGPFLGWLRLQHLGL---		
IGFBP	SHNRLAELPADALGPLQRAFWLDVSHNRL-----EALPGSLLASLGRLR-YLNL---		

Fig. 26B

	601	660
human LRSG-1	REGNLPILLIAPALAAVLLAALAAGAAAY-CVRRGRAMAAAAQDKGQVGPAGAGPLELEGVK	
murine LRSG-1	REGNLPILLIAPALAAVLLAVLAAAGAAAY-CVRRARA-TSTAQDKGQVGPAGTGPLELEGVK	
GPV	VGGEPPRCAGPGAAGLPLWALPGDAECPPGPPPPRPAADSSSEAP-----VH	
IGFBP	R--NNSLRITFTPPGGLERLN-LEGPFWDSCPLKALRDFALQNPSAVP-----R-	
	661	720
human LRSG-1	VPLEPGPKATEGGGEALPSGS-ECEVPLMGF-----PGPGLQSP-----L	
murine LRSG-1	APLEPGSKATEGGGEALSGBP-ECEVPLMGY-----PGPSLQGV-----L	
GPV	PALAPNSSEPWWAQPVTTGKGQDHSFPGFYFLLAVQAMITVIITVFAMIKIGQLFRKL	
IGFBP	-----FVQAICEG-DDCQPPVYTYNNITCASPPEVAGLDL-----RDL	
	721	728
human LRSG-1	HAKPYI--	
murine LRSG-1	PAKHYI--	
GPV	IRER-ALG	
IGFBP	GEAHFAPC	

Fig. 26C

60/68

GAATTCCCGGGTCGACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGGCTGAGCGAAGCGCGGCGGCGGCGGCGG 79  
CGCCTAGGGGAGGGAGGGGCGGCGGGGCCGAGCCCACCTAGCGGAGCGCGCCGGCCGCGCGGTGGCCGCGCCAGCATGC 158  
CCCCGCCCCGCGGCGCGCTCCGCGGCCAGCCACCCCCGCGGCCCTCGGCGGGCCTGCGCTCGGCCCGGGGGCGCGGGAACC 237  
GCAGCCGAGCCCGAGGCGGGAGCAGCGAGCCCGGAGCCCCGGGCGCTCGAATGCAGGATGCTCGTGGTCCCCAGCATCC 316  
TTGAGCCACCAGGAGTGAGGGCTGCTGCTCCCTGAGACCTGGCTCCAAGGAGGATGCCACAGCCGCTGCCAGCTCCGG 395  
  
M S D E R R L P G S A V G W L V C 17  
TCTGCACC ATG AGT GAT GAG CGG CGG CTG CCT GGC AGT GCA GTG GGC TGG CTG GTA TGT 454  
  
G G L S L L A N A W G I L S V G A K Q K 37  
GGG GGC CTC TCC CTG CTG GCC AAT GCC TGG GGC ATC CTC AGC GTT GGC GCC AAG CAG AAG 514  
  
K W K P L E F L L C T L A A T H M L N V 57  
AAG TGG AAG CCC TTG GAG TTC CTG CTG TGT ACG CTC GCG GCC ACC CAC ATG CTA AAT GTG 574  
  
A V P I A T Y S V V Q L R R Q R P D F E 77  
GCC GTG CCC ATC GCC ACC TAC TCC GTG GTG CAG CTG CGG CGG CAG CGC CCC GAC TTC GAG 634  
  
W N E G L C K V F V S T F Y T L T L A T 97  
TGG AAT GAG GGT CTC TGC AAG GTC TTC GTG TCC ACC TTC TAC ACC CTC ACC CTG GCC ACC 694  
  
C F S V T S L S Y H R M W M V C W P V N 117  
TGT TTC TCT GTC ACC TCC CTC TCC TAC CAC CGC ATG TGG ATG GTC TGC TGG CCT GTC AAC 754  
  
Y R L S N A K K Q A V H T V M G I W M V 137  
TAC CGG CTG AGC AAT GCC AAG AAG CAG GCG GTG CAC ACA GTC ATG GGT ATC TGG ATG GTG 814  
  
S F I L S A L P A V G W H D T S E R F Y 157  
TCC TTC ATC CTG TCG GCC CTG CCT GCC GTT GGC TGG CAC GAC ACC AGC GAG CGC TTC TAC 874  
  
T H G C R F I V A E I G L G F G V C F L 177  
ACC CAT GGC TGC CGC TTC ATC GTG GCT GAG ATC GGC CTG GGC TTT GGC GTC TGC TTC CTG 934  
  
L L V G G S V A M G V I C T A I A L F Q 197  
CTG CTG GTG GGC GGC AGC GTG GCC ATG GGC GTG ATC TGC ACA GCC ATC GCC CTC TTC CAG 994  
  
T L A V Q V G R Q A D H R A F T V P T I 217  
ACG CTG GCC GTG CAG GTG GGG CGC CAG GCC GAC CAC CGC GCC TTC ACC GTG CCC ACC ATC 1054  
  
V V E D A Q G K R R S S I D G S E P A K 237  
GTG GTG GAG GAC GCG CAG GGC AAG CGG CGC TCC TCC ATC GAT GGC TCG GAG CCC GCC AAA 1114  
  
T S L Q T T G L V T T I V F I Y D C L M 257  
ACC TCT CTG CAG ACC ACG GGC CTC GTG ACC ACC ATA GTC TTC ATC TAC GAC TGC CTC ATG 1174  
  
G F P V L D S T P I P E R S A V R Q G E 277  
GGC TTC CCT GTG CTG GAC TCT ACG CCC ATC CCC GAA AGG TCT GCA GTG AGA CAG GGA GAG 1234  
  
D W G K D Q P E G F H P S S R Q D C L P 297  
GAC TGG GGC AAA GAC CAG CCT GAG GGG TTT CAT CCA AGC AGC AGG CAA GAC TGC CTT CCC 1294

\*  
TGA

298  
1297

Fig. 27A

GCCATTGCAGGACATGAGGACATGAGCTCCAGAATGGTGCCAGGCCGAGCCCTGTGCCCACAGGTGGTGAGCTTCAGCA 1376  
GCCTGCGGGCCGACGCCTCAGCGCCCTGGATGGCACTCTGCGTGCTGTGGTGCTCCGTGGCCCAGGCCCTGCTTCCGAC 1455  
CTGTCCTGCCTCAGTTTCCCCATCTGTGATGAGCAGGTGACCACGTTAACTCTCAGGGCTGTTTGAAGTCTCTTGGTTG 1534  
TAGGCCCTCGCCACTGAGTGGCCCAGGTGTGAGAGGTAGTCTAGAGCCCTCTGCGGCCTTTGTGGAGGTCCGTTCTCAG 1613  
CATGTGGCCTGGTGTGGCTCCCTAGGCCTGAGGCCTCCCACTCTCAGTGCCCCCTGCCCCCTTGGGAACCCACACTCCA 1692  
CCCCAGCTAAGCACAACTGTGGACCACCACCAATGGCACCTGAGCCACCTTGACCACCAATTAGTGTCCCCACCCCTCA 1771  
TTACTCTGCCGTCGTTGCCTGTCCCCACCACATCATCTCCCTCCATGGCTCCCAACCATGACGCTGGCAGGTGCAAGCGG 1850  
AGAGCACGAGGGCAGCAGGGCCTGGCCTTCCGTGTCCCTGCGTCATCCCCAGCCTCACTCCCCACCCGTGCAGGCCTGG 1929  
CCAGGAAGGGATCCTGGCAGGGGCTTCCAGGTTCTCAGCTCAAGGCCTGGTCCCGGGCAGGCGTCCAACCCCTGGGAGC 2008  
AATGTATTTCTTTGCCTTCCATCCTGGGCAGACCCCTTACAGGCCTGGGCATTGCCATGGGGCCCTGGGTCTTCCCAGGC 2087  
TAAGGAGAACCAGGAACAGCTATAACCTTGAGCTAGTGAAATAGGGTAGATGAGAAGGCTGTCTCTCCAGACCCCTAC 2166  
CCCTACACAGTGGCCCCACAATATGAAGACCTGGGGTAATTCCAAGGTGAGCATAGAGCCTGCCTGTGCCCAGTTCCTT 2245  
CTGGCCCTCAGGTGGCCAAGCCCATCTCTTCATCCTTCAGATAGGGTCCCACTCCAGAAGAAGCTGCTGGGGTGGGGG 2324  
TGGGAGGCTGCCTAAGCCTGTCTGTGCTTCAGAGGCCCCCTCCAGTCCCTGGCTGTGGGGTAACTGGGGGTATGAGCTGT 2403  
GGCCACAGGTGAGCAAGGCAGGGAAGTCAATCCAGCCCTGGCCGCGGGAGGGGCCATCTCTGGCCAATGCTGCTGTGC 2482  
CTTCAAGGACTGACAAGTTACGTAGGGGCAGAGGTCGCCAGCTAGCCAGTGTCTCCTCCATCTGGGGGGCGTCTGTCCA 2561  
CTTGTCACCTTAGGTTTTCACTCATTTGTACCTTGGGGTTTTGCTCTGTGTGTTTCATATCCAACGGCAATACTTGCA 2640  
GGGGGACAGAGTCTCTAAATACTCCAATCCTGCGTTTTTTACAAACATAAAGGGGGAGACCCCAAGTGGAGGACCCTG 2719  
GGCCTGGAGCTCCCTCCCAAACCTTTGTCCAGCATCCAGCCTGTTCCCTGGGCTCACTGGGGAGGGAGTTGTCTTCATAG 2798  
CACACCCAGAGCCAGGGATCCCTTTGTAGTTTTTTTGACAACGGAGCATTTCTCTTCTGTACAGGACCCAATAAAAACTT 2877  
CCTTATGATTTGCAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2915

Fig. 27B

GAATTCCCGGGTCGACCCACGCGTCCGGCGGGCGGGGCCGAGCCACCTAGCGGAGCGCGCCGGCCCGCGGTGGCCGCCG	79
CCAGCATGCCCCGGCCCCGCGGGCCGCTCCGCCGCCAGCCACCCCCGCGGCCCTCGGCGGCCCTGCGCTCGGCCCGGGGGC	158
GCGGGAACCGCAGCCCGAGCCCGGAGGCGGGAGCAGCGAGCCCGAGCCCCGGGCGCTCGAATGCAGGATGCTCGTGGTCC	237
CCAGCATCCTTGAGCCACCAGGAGTGAGGGCTGCTGCTCCCTGAGACCTGGCTCCAAGGAGGATGCCACAGCCGCTGC	316
M S D E R R L P G S A V G W L	15
CAGCTCCGGTCTGCACC ATG AGT GAT GAG CGG CGG CTG CCT GGC AGT GCA GTG GGC TGG CTG	378
V C G G L S L L A N A W G I L S V G A K	35
GTA TGT GGG GGC CTC TCC CTG CTG GCC AAT GCC TGG GGC ATC CTC AGC GTT GGC GCC AAG	438
Q K K W K P L E F L L C T L A A T H M L	55
CAG AAG AAG TGG AAG CCC TTG GAG TTC CTG CTG TGT ACG CTC GCG GCC ACC CAC ATG CTA	498
N V A V P I A T Y S V V Q L R R Q R P D	75
AAT GTG GCC GTG CCC ATC GCC ACC TAC TCC GTG GTG CAG CTG CGG CGG CAG CGC CCC GAC	558
F E W N E G L C K V F V S T F Y T L T L	95
TTC GAG TGG AAT GAG GGT CTC TGC AAG GTC TTC GTG TCC ACC TTC TAC ACC CTC ACC CTG	618
A T C F S V T S L S Y H R M W M V C W P	115
GCC ACC TGT TTC TCT GTC ACC TCC CTC TCC TAC CAC CGC ATG TGG ATG GTC TGC TGG CCT	678
V N Y R L S N A K K Q A V H T V M G I W	135
GTC AAC TAC CGG CTG AGC AAT GCC AAG AAG CAG GCG GTG CAC ACA GTC ATG GGT ATC TGG	738
M V S F I L S A L P A V G W H D T S E R	155
ATG GTG TCC TTC ATC CTG TCG GCC CTG CCT GCC GTT GGC TGG CAC GAC ACC AGC GAG CGC	798
F Y T H G C R F I V A E I G L G F G V C	175
TTC TAC ACC CAT GGC TGC CGC TTC ATC GTG GCT GAG ATC GGC CTG GGC TTT GGC GTC TGC	858
F L L L V G G S V A M G V I C T A I A L	195
TTC CTG CTG CTG GTG GGC GGC AGC GTG GCC ATG GGC GTG ATC TGC ACA GCC ATC GCC CTC	918
F Q T L A V Q V G R Q A D H R A F T V P	215
TTC CAG ACG CTG GCC GTG CAG GTG GGG CGC CAG GCC GAC CAC CGC GCC TTC ACC GTG CCC	978
T I V V E D A Q G K R R S S I D G S E P	235
ACC ATC GTG GTG GAG GAC GCG CAG GGC AAG CGG CGC TCC TCC ATC GAT GGC TCG GAG CCC	1038
A K T S L Q T T G L V T T I V F I Y D C	255
GCC AAA ACC TCT CTG CAG ACC ACG GGC CTC GTG ACC ACC ATA GTC TTC ATC TAC GAC TGC	1098
L M G F P V L V V S F S S L R A D A S A	275
CTC ATG GGC TTC CCT GTG CTG GTG GTG AGC TTC AGC AGC CTG CGG GCC GAC GCC TCA GCG	1158
P W M A L C V L W C S V A Q A L L L P V	295
CCC TGG ATG GCA CTC TGC GTG CTG TGG TGC TCC GTG GCC CAG GCC CTG CTG CTG CCT GTG	1218
F L W A C D R Y R A D L K A V R E K C M	315
TTC CTC TGG GCC TGC GAC CGC TAC CGG GCT GAC CTC AAA GCT GTC CGG GAG AAG TGC ATG	1278
A L M A N D E E S D D E T S L E G G I S	335
GCC CTC ATG GCC AAC GAC GAG GAG TCA GAC GAT GAG ACC AGC CTG GAA GGT GGC ATC TCC	1338

Fig. 28A

63/68

P	D	L	V	L	E	R	S	L	D	Y	G	Y	G	G	D	F	V	A	L	355
CCG	GAC	CTG	GTG	TTG	GAG	CGC	TCC	CTG	GAC	TAT	GGC	TAT	GGA	GGT	GAT	TTT	GTG	GCC	CTA	1398
D	R	M	A	K	Y	E	I	S	A	L	E	G	G	L	P	Q	L	Y	P	375
GAT	AGG	ATG	GCC	AAG	TAT	GAG	ATC	TCC	GCC	CTG	GAG	GGG	GGC	CTG	CCC	CAG	CTC	TAC	CCA	1458
L	R	P	L	Q	E	D	K	M	Q	Y	L	Q	V	P	P	T	R	R	F	395
CTG	CGG	CCC	TTG	CAG	GAG	GAC	AAG	ATG	CAA	TAC	CTG	CAG	GTC	CCG	CCC	ACG	CGG	CGC	TTC	1518
S	H	D	D	A	D	V	W	A	A	V	P	L	P	A	F	L	P	R	W	415
TCC	CAC	GAC	GAT	GCG	GAC	GTG	TGG	GCC	GCC	GTC	CCG	CTG	CCC	GCC	TTC	CTG	CCG	CGC	TGG	1578
G	S	G	E	D	L	A	A	L	A	H	L	V	L	P	A	G	P	E	R	435
GGC	TCC	GGC	GAG	GAC	CTG	GCC	GCC	CTG	GCG	CAC	CTG	GTG	CTG	CCT	GCC	GGG	CCC	GAG	CGG	1638
R	R	A	S	L	L	A	F	A	E	D	A	P	P	S	R	A	R	R	R	455
CGC	CGC	GCC	AGC	CTC	CTG	GCC	TTC	GCG	GAG	GAC	GCA	CCA	CCG	TCC	CGC	GCG	CGC	CGC	CGC	1698
S	A	E	S	L	L	S	L	R	T	S	A	L	D	S	G	P	R	G	A	475
TCG	GCC	GAG	AGC	CTG	CTG	TCG	CTG	CGG	ACC	TCG	GCC	CTG	GAT	AGC	GGC	CCG	CGG	GGA	GCC	1758
R	D	S	P	P	G	S	P	R	R	R	P	G	P	G	P	R	S	A	S	495
CGC	GAC	TCG	CCC	CCC	GGC	AGC	CCG	CGC	CGC	CGC	CCC	GGG	CCC	GGC	CCC	CGC	TCC	GCC	TCG	1818
A	S	L	L	P	D	A	F	A	L	T	A	F	E	C	E	P	Q	A	L	515
GCC	TCG	CTG	CTG	CCC	GAC	GCC	TTC	GCC	CTG	ACC	GCC	TTC	GAG	TGC	GAG	CCA	CAG	GCC	CTG	1878
R	R	P	P	G	P	F	P	A	A	P	A	A	P	D	G	A	D	P	G	535
CGC	CGC	CCG	CCC	GGG	CCC	TTC	CCC	GCT	GCG	CCC	GCC	GCC	CCC	GAC	GGC	GCA	GAT	CCC	GGA	1938
E	A	P	T	P	P	S	S	A	Q	R	S	P	G	P	R	P	S	A	H	555
GAG	GCC	CCG	ACG	CCC	CCA	AGC	AGC	GCC	CAG	CGG	AGC	CCA	GGG	CCA	CGC	CCC	TCT	GCG	CAC	1998
S	H	A	G	S	L	R	P	G	L	S	A	S	W	G	E	P	G	G	L	575
TCG	CAC	GCC	GGC	TCT	CTG	CGC	CCC	GGC	CTG	AGC	GCG	TCG	TGG	GGC	GAG	CCC	GGG	GGG	CTG	2058
R	A	A	G	G	G	S	T	S	S	F	L	S	S	P	S	E	S	S		595
CGC	GCG	GCG	GGC	GGC	GGC	AGC	ACC	AGC	AGC	TTC	CTG	AGT	TCC	CCC	TCC	GAG	TCC	TCG		2118
G	Y	A	T	L	H	S	D	S	L	G	S	A	S	*						610
GGC	TAC	GCC	ACG	CTG	CAC	TCG	GAC	TCG	CTG	GGC	TCC	GCG	TCC	TAG						2163
GACCGCCGGCGCCTCCCCACGGACGCCAGGCAGGCCAGGCCGCTCTCCGGGGCCGACAGCACCAAAGACGCCCGCCTCCC																				2242
CCCCGCGCGCAGACATGCGCCACCCCTCCAGGGGTGAGGGGGCGTTGGCCTCAGCGTTTGTCTTCCGGCTCCTCCCAG																				2321
CTGGCCTTTGTCCCAGGGGGCAGCGGCTGCCCCGACGACTGCGCTGGGCACCGCATGTCCCAGGGCCGAGTGAGGTGCGGC																				2400
CTGGGGAGCTGAGTGACATCCCAAGCTTGGGCTTGGGTAGTGAGTGACATGTGCACACGTCCAGCTGCGCCATCACCAG																				2479
CCCTGCGCAACAGGACGTCCGGAGCAGGGAACCTGAGACAGGGCCACTGCGGGATCGGACAAAGCCCCGCTTTGGAGAG																				2558
GCTGAGCTGGAGCCATTGGCCTCCCCAGGGGCTTTCCACCCACACTGCACCATAACCGCCACACCCTTCGGGGGGGGGG																				2637
AGGGTACAGAGGGTCTCTAAGCACAGGGGTGTTTCAGAGCCCCGAACAAGCTTTGATCAGGTTTCCCTGCTTCCGACCTGT																				2716
CCTGCCTCAGTTTCCCCATCTGTGATGAGCAGGTGACCACGTAACTCTCAGGGCTGTTTGAAGTCTCTTGGTTGTAGG																				2795

Fig. 28B

CCCTCGCCACTGAGTGGCCCAGGTGTGAGAGGTAGTCTAGAGCCCTCTGCGGCCTTTGTGGAGGTCCGTTCTCAGCATG 2874

TGGCCTGGTGTGGCTCCCTAGGCCTGAGGCCTCCCACTCTCAGTGCCCCCTGCCCCCTTGGGAACCCCACTCCACCCC 2953

AGCTAAGCACAACTGTGGACCACCACCAATGGCACCTGAGCCACCTTGACCACCATTAGTGTCCCCACCCTCATTAC 3032

TCTGCCGTCGTTGCCTGTCCCCACCACATCATCTCCCTCCATGGCTCCCACCATGACGCTGGCAGGTGCAAGCGGAGAG 3111

CACGAGGGCAGCAGGGCCTGGCCTTCCGTGTCCCTGCGTCATCCCCAGCCTCACTCCCCACCCGTGCAGGCCTGGCCAG 3190

GAAGGGATCCTGGCAGGGGCTTCCAGGTTCTCAGCTCAAGGCCTGGTCCCGGGCAGGCGTCCAACCCCTGGGAGCAATG 3269

TATTTCTTTGCCTTCCATCCTGGGCAGACCCCTTACAGGCCTGGGCATTGCCATGGGCCCCTGGGTCTTCCCAGGCTAAG 3348

GAGAACCAGGAACAGCTATAACCTTGAGCTAGTGAAATAGGGTAGATGAGAAGGCTGTCTCCTCCAGACCCCTACCCCT 3427

ACACAGTGGCCCCACAATATGAAGACCTGGGGTAATTCCAAGGTGAGCATAGAGCCTGCCTGTGCCAGTTCTTTCTGG 3506

CCCTCAGGTGGCCAAGCCCATCTCTTCATCCTTCAGATAGGGTCCCACTCCCAGAAGAAGCTGCTGGGGTGGGGGTGGG 3585

AGGCTGCCTAAGCCTGTCTGTGCTTCAGAGGCCCTCCAGTCCCTGGCTGTGGGGTAACTGGGGGTATGAGCTGTGGCC 3664

ACAGGTGAGCAAGGCAGGGAAGTGAATCCAGCCCTGGCCGCGGGAGGGGCCATCTCTGGCCAATGCTGCTGTGCCTTC 3743

AAGGACTGACAAGTTACGTAGGGGCAGAGGTCGCCAGCTAGCCAGTGTCTCCTCCATCTGGGGGGCGTCTGTCCACTTG 3822

TCACCTTAGGTTTTCACCTCATTTGTACCTTGGGGTTTGTCTGTGTGTTTCATATCCAACGGCAATACTTGCAGGGG 3901

GACAGAGTCCTCTAAATACTCCAATCCTGCGGTTTTTACAAACATAAAGGGGGAGACCCAAGTGGAGGACCCTGGGCC 3980

TGGAGCTCCCTCCCAAACTTTGTCCAGCATCCAGCCTGTTCCTGGGCTCACTGGGGAGGGAGTTGTCTTCATAGCACA 4059

CCCAGAGCCAGGGATCCCTTTGTAGTTTTTTGACAACGGAGCATTTCTCTTCTGTACAGGACCCAATAAAAACTTCCTT 4138

ATGAAAAAAAAAAAAAAAAAGGGCGGCCGC 4166

Fig. 28C



65/68

	1	60
SSTM-1	MS-----DERRLPGS <u>AVGWL</u> VCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHM	
SSTM-2	MS-----DERRLPGS <u>AVGWL</u> VCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHM	
proteinA-2	MARGGAGAEELSRNALSWLACGLLALLANAWIILSISAKQKKHKLLELLCFLAGTHI	
proteinA-3	-----	
	61	120
SSTM-1	<u>LNAVPIATYSVVQLRRQ</u> -RPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVC	
SSTM-2	<u>LNAVPIATYSVVQLRRQ</u> -RPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVC	
proteinA-2	LMAAVPLTTFVVQLRRQASSDYDNESICKVFVSTFYTLALATCFVASLSYHRMWMVR	
proteinA-3	-----	
	121	180
SSTM-1	<u>WPVNYRLSNAKKQAVHTVMGIWMVSFILSALPAVGWHD</u> TSEFYTHGCRFIVAEIGLGFG	
SSTM-2	<u>WPVNYRLSNAKKQAVHTVMGIWMVSFILSALPAVGWHD</u> TSEFYTHGCRFIVAEIGLGFG	
proteinA-2	WPVNYRLSNAKKQALHAVMGIWMVSFILSTLPSIGWHNNGERYYARGCQFIVSKIGLGFG	
proteinA-3	-----	
	181	240
SSTM-1	<u>VCFLLL</u> VGGSVAMGVICTAIALFQTL-----AVQVGRQADHRAFT	
SSTM-2	<u>VCFLLL</u> VGGSVAMGVICTAIALFQTL-----AVQVGRQADHRAFT	
proteinA-2	VCFSLLLLGGIVMGLVCVAITFYQTLWARPRRARQARRVGGGGGTKAGGPGALGTRPAFE	
proteinA-3	-----ITFYQTLWARPRRARQARRVGGGGGTKAGGPGALGTRPAFE	
	241	300
SSTM-1	VPTIVVEDAQGKRRSSIDGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL-----	
SSTM-2	VPTIVVEDAQGKRRSSIDGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVLVVSFSSLRADA	
proteinA-2	VPAIVVEDARGKRRSSLDGSEAKTSLQVTNLVSAIVFLYDSLTVGPILVVSFFSLKSDS	
proteinA-3	VPAIVVEDARGKRRSSLDGSEAKTSLQVTNLV-----VSFFSLKSDS	
	301	360
SSTM-1	-----DSTPI---	
SSTM-2	<u>SAPWMALCVLWCSVAQALLPVFLWACDRYRADLKAVREKCMALMANDEESDDETSLEGG</u>	
proteinA-2	APPWMVLAVLWCSMAQTLLLPSFIWSCERYRADVRTVWEQCVAIMSEEDGDDD-----G	
proteinA-3	APPWMVLAVLWCSMAQTLLLPSFIWSCERYRADVRTVWEQCVAIMSEEDGDDD-----G	
	361	420
SSTM-1	-----P	
SSTM-2	<u>ISPDVL</u> LER--SLDYGYGDFVALDRMAKYEISALEGGLPOLYPLRPLQEDKMQYLQVPP	
proteinA-2	GCDDYAEGRVCKVRFDANGATGPGSRDPA-QVKLLPGR-HMLFP--PL--ERVHYLQVPL	
proteinA-3	GCDDYAEGRVCKVRFDANGATGPGSRDPA-QVKLLPGR-HMLFP--PL--ERVHYLQLK-	
	421	480
SSTM-1	ERSAVRQGED-----WGKDQ-----	
SSTM-2	TRRFSHDDADVWAAVPLPA-FLPRWGSGEDLAALHLVLP-AGPERRRASLLAFAEDAPP	
proteinA-2	SRRLSHDETNIFFSTPREPGSFLHKWSSSDDIRVLPAQSRALGGPPEYLQQRHLEDEEDE	
proteinA-3	KLDLAAAAAHTF-----FVANPMHLQ-----	
	481	540
SSTM-1	-----PEGFH-----	
SSTM-2	SRARRRSAESLLSLRTSALDSGPRGARDSPPGSPRRRPGPGPRASASALLPDAFALTAFE	
proteinA-2	EEA---EGGGLASLRQF-LESGVLGSGGGPP-----RGPG-----FFRE--EITTF-	
proteinA-3	-----MRE--DMAKY-	

Fig. 29A

	541		600
SSTM-1	-----PSSRQ-----		
SSTM-2	CEPQALRRPPGPFPAAPADGADPGEAPTPPSSAQRSPGPRP--SAHSHAGSLRPGLSA		
proteinA-2	-----IDETPLPSPTASPGHSPRRPRPLGLSPRRLSLGSPESRAVGLPLGLSA		
proteinA-3	-----RRMS-----		
	601	642	
SSTM-1	-----DCL---	P	
SSTM-2	SWGEPGGLRAAGGGGSTSSFLSSPSESSGYATLHSDSLGSAS		
proteinA-2	-----GRRCSLTGGEESARAWGGSWGPGNPIFPQLTL----		
proteinA-3	-----GVR-----		

Fig. 29B

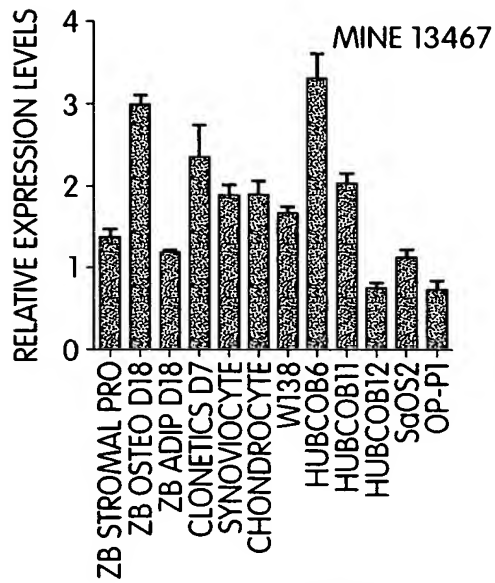


Fig. 30A

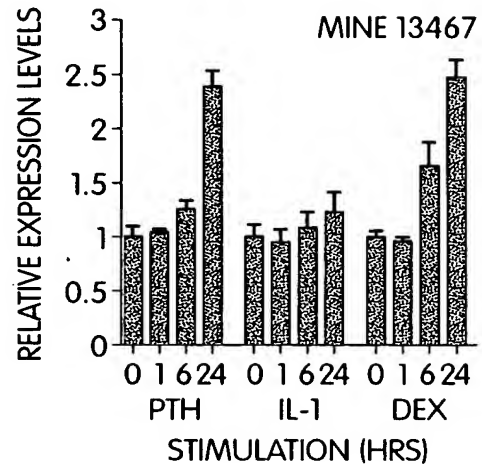


Fig. 30B

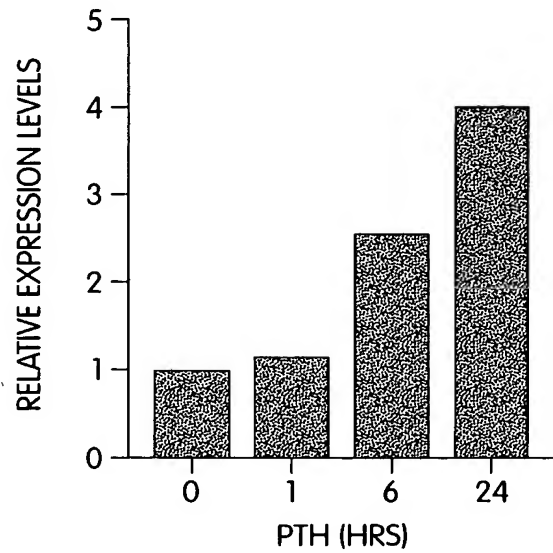


Fig. 30C

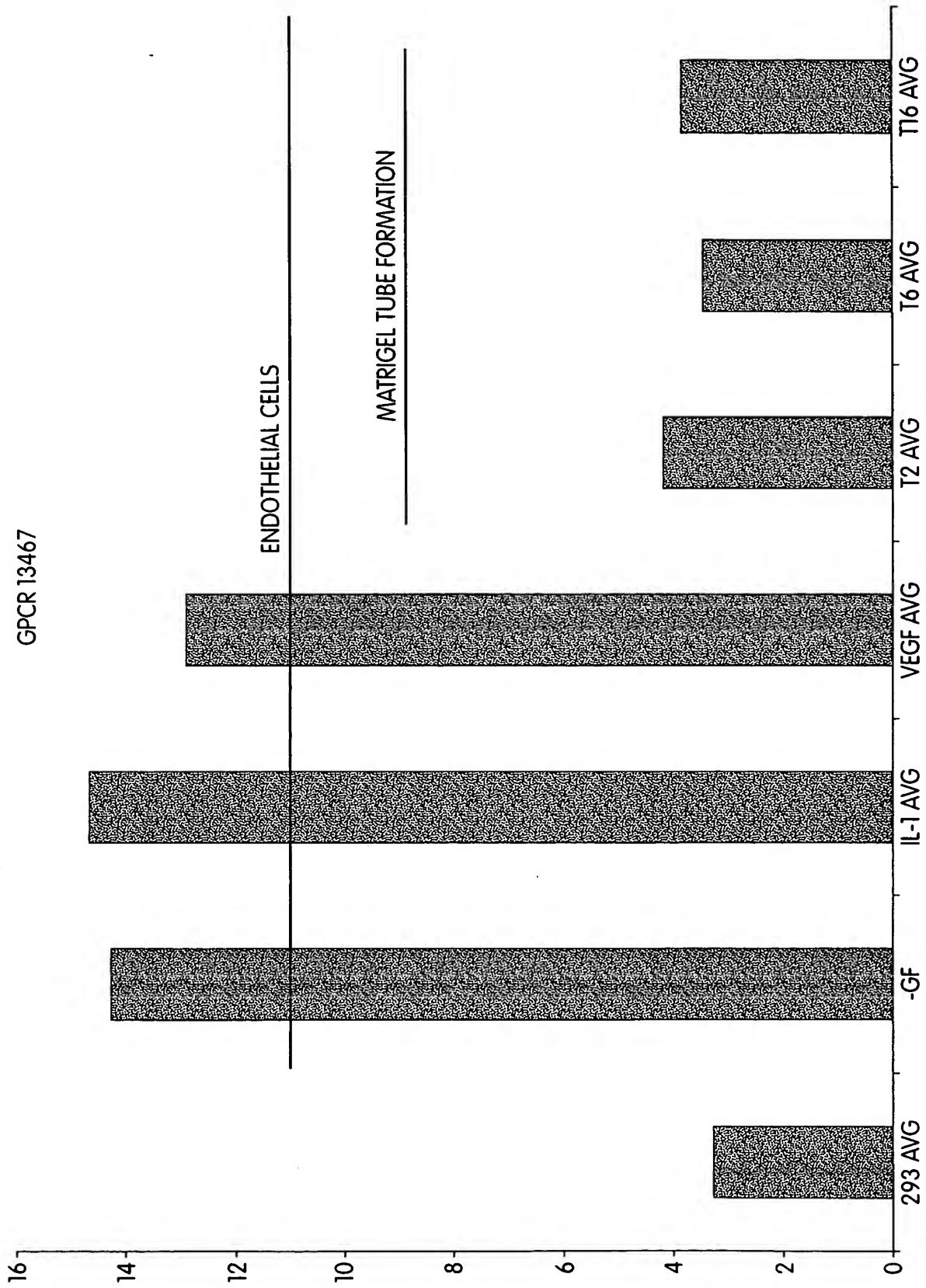


Fig. 31